

Mon Aug 30 08:48:58 2004

us-09-914-883-2.aug04.fai

Page 1

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CM protein - protein search, using sw model

Run on: August 28, 2004, 04:05:25 ; Search time 23.186 Seconds  
(without alignments)  
2195.179 Million cell updates/sec

Title: US-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MALRGLGALLLPPLAIVE.....ILNSIQWRAQNNQIQSEV 986

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5130	98.9	994	3	US-08-542-635-2
2	5093	98.2	970	2	US-08-449-643A-11
3	5093	98.2	970	2	US-08-702-367A-11
4	5093	98.2	970	5	PCT-US95-04681-11
5	4993.5	96.3	995	1	US-08-162-809-18
6	4971.5	95.8	1011	1	US-08-162-809-12
7	4962.5	95.7	995	2	US-08-673-789-5

#### ALIGNMENTS

RESULT 1  
US-08-542-635-2  
; Sequence 2, Application US/08542635  
; Patent No. 6218356  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; APPLICANT: Letwin, Kenneth  
; TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Berezkin & Parr  
; STREET: 40 King Street West, Box 401  
; CITY: Toronto

QY	10	LLLPPLAAYETIMDTATATETAGMWHPPSGMEVSGYDENMNTIRTYOVNPFESSQ	69
DB	18	LLLPPLAAYETIMDTATATETAGMWHPPSGMEVSGYDENMNTIRTYOVNPFESSQ	77
QY	70	NNMLRTFIRRCGRHRIHVMKRSVDCSSIBSVPSCKETPNLYYYEADPDSATKTFPN	129
DB	78	NNMLRTFIRRCGRHRIHVMKRSVDCSSIBSVPSCKETPNLYYYEADPDSATKTFPN	137
QY	130	WMENPWKVDITIADEFSQVDLGGRYMKINTVRSFGVRSRGFYLAQDYGGCMLIA	189
DB	138	WMENPWKVDITIADEFSQVDLGGRYMKINTVRSFGVRSRGFYLAQDYGGCMLIA	197
QY	190	VRYFYRKCPRILIONGALFQETLSGABSTSLVARGSCINAEVDPITLYCNGDEMLV	249
DB	198	VRYFYRKCPRILIONGALFQETLSGABSTSLVARGSCINAEVDPITLYCNGDEMLV	257
QY	250	PIGRCKAGFEAVENGTVCRGCPGTFKANGDEACTHCPINRSTTSKATNCVRCNGY	309
DB	258	PIGRCKAGFEAVENGTVCRGCPGTFKANGDEACTHCPINRSTTSKATNCVRCNGY	317
QY	310	YRADLDPLDMPCTTIPAPQAVISSVNETSLMELMTPRDSGREDLVNIIICKSGSGR	369
DB	318	YRADLDPLDMPCTTIPAPQAVISSVNETSLMELMTPRDSGREDLVNIIICKSGSGR	377
QY	370	GACTRCGDNVQYAPROGLTEPRITYISDLIAHTQYFELIOAVNGVQDPSFQFASVNI	429
DB	378	GACTRCGDNVQYAPROGLTEPRITYISDLIAHTQYFELIOAVNGVQDPSFQFASVNI	437
QY	430	TTNOAASVSIHMOVSRITVDSITLSMSQPDQNGVILDOYELQYKEKSEVYATIKSP	489
DB	438	TTNOAASVSIHMOVSRITVDSITLSMSQPDQNGVILDOYELQYKEKSEVYATIKSP	497

QY 490 INTVTVOGKAGAIYFQVRAITVAGYGRYSGKMYFQMTAEAYOTSIOEKLPLIIGSSA 549  
Db 498 INTVTVOGKAGAIYFQVRAITVAGYGRYSGKMYFQMTAEAYOTSIOEKLPLIIGSSA 557  
QY 550 AGVLLIVVYAIACNRRGFERADSEYTDLOHTSGHMTPKMKIYIDPPTYEDPNEAV 609  
Db 558 AGVLLIVVYAIACNRRGFERADSEYTDLOHTSGHMTPKMKIYIDPPTYEDPNEAV 617  
QY 610 REFAPKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFAIAIKTLKSGYTEKORRDFLS 669  
Db 618 REFAPKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIIFAIAIKTLKSGYTEKORRDFLS 677  
QY 670 EASIMGQPDHPNVVHLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDGQFTYIQLVGMKRG 729  
Db 678 EASIMGQPDHPNVVHLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDGQFTYIQLVGMKRG 737  
QY 730 IAAKMKYLDNMVYHRDLAARNILVNSLVCKVSDFGLSRFLBEDTSDPTTYTSLGSKIP 789  
Db 738 IAAKMKYLDNMVYHRDLAARNILVNSLVCKVSDFGLSRFLBEDTSDPTTYTSLGSKIP 797  
QY 790 IRMTAPPELQYRKRTSASDVMSYGIIVMVEVNSYGERPYWDMTNDVINAIEQDYRLPPEM 849  
Db 798 IRMTAPPELQYRKRTSASDVMSYGIIVMVEVNSYGERPYWDMTNDVINAIEQDYRLPPEM 857  
QY 850 DCPBALHQLMDQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRT 909  
Db 858 DCPBALHQLMDQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRT 917  
QY 910 PDYTSFNTVDBWLEAIKMGQYKESFANAGFTSPDYVSQMMMEDILRLGVTLAAGHKKIIN 969  
Db 918 PDYTSFNTVDBWLEAIKMGQYKESFANAGFTSPDYVSQMMMEDILRLGVTLAAGHKKIIN 977  
QY 970 SIQVRAQNMQIOSVEV 986  
Db 978 SIQVRAQNMQIOSVEV 994

RESULT 2  
US-08-449-645A-11  
Sequence 11, Application US/08449645A  
Patent No. 5981245  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1640 Dehaven Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-449-645A-11

Query Match 98.2%; Score 5093; DB 2; Length 970;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 15 LAAVETLMDSTTATAEIGMMVHPSPGMEESGYDENNNITRTYQVCFVSSQNNMLR 74  
Db 1 LAAVETLMDSTTATAEIGMMVHPSPGMEESGYDENNNITRTYQVCFVSSQNNMLR 60  
QY 75 TKFIRRRGHRHVMKRSVRCCSSIPSPGCKETNULYYEADFDSATKTFPMWENP 134  
Db 61 TKFIRRRGHRHVMKRSVRCCSSIPSPGCKETNULYYEADFDSATKTFPMWENP 120  
QY 135 WKVVDITIADESFSQVDLGRVMKINTEVRSGFYPYRSGFYAFODYGGCSMLIVRYFY 194  
Db 121 WKVVDITIADESFSQVDLGRVMKINTEVRSGFYPYRSGFYAFODYGGCSMLIVRYFY 180  
QY 195 RCPRIITQNGAIFQETLSGASTSIVAAKSGCIANAEEVDYPIKLYCNGDEMTVPIGR 254  
Db 181 RCPRIITQNGAIFQETLSGASTSIVAAKSGCIANAEEVDYPIKLYCNGDEMTVPIGR 240  
QY 255 MCKAGFEAVENGTVGRGCPSTFRKANQDEACTHCPIRSRTTSGATNCVCRNGYRADL 314  
Db 241 MCKAGFEAVENGTVGRGCPSTFRKANQDEACTHCPIRSRTTSGATNCVCRNGYRADL 300  
QY 315 DPLDMPCTTISAPQAVISSVNETSLMLEWTPPPDSGGRDLVYNIICSGSGRGACTR 374  
Db 301 DPLDMPCTTISAPQAVISSVNETSLMLEWTPPPDSGGRDLVYNIICSGSGRGACTR 360  
QY 375 CGDNVQYAPRQGLTEPRYISDLAHTQYFEEIQAVNGVTDGSPSPQFASVNTTNOA 434  
Db 361 CGDNVQYAPRQGLTEPRYISDLAHTQYFEEIQAVNGVTDGSPSPQFASVNTTNOA 420  
QY 435 APSAVSIHQVSRVDSITLWSQPDQPNVYLDLQYKEKLESEYNATAIKSPNTVT 494  
Db 421 APSAVSIHQVSRVDSITLWSQPDQPNVYLDLQYKEKLESEYNATAIKSPNTVT 480  
QY 495 VQGLKAGAIYFQVRAITVAGYGRYSGKMYFQMTAEAYOTSIOEKLPLIIGSSAGLV 554  
Db 481 --GLKAGAIYFQVRAITVAGYGRYSGKMYFQMTAEAYOTSIOEKLPLIIGSSAGLV 538  
QY 555 LIAVVVIAICNRRGFERADSEYTDLOHTSGHMTPKMKIYIDPPTYEDPNEAVFEAK 614  
Db 539 LIAVVVIAICNRRGFERADSEYTDLOHTSGHMTPKMKIYIDPPTYEDPNEAVFEAK 598  
QY 615 EIDISCVKIQVIGAGEFGEVCSGHLKLPKREIIFAIAIKTLKSGYTEKORRDFLSASIM 674  
Db 599 EIDISCVKIQVIGAGEFGEVCSGHLKLPKREIIFAIAIKTLKSGYTEKORRDFLSASIM 658  
QY 675 GQPDHPNVVHLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDGQFTYIQLVGMKRGIAAGM 734  
Db 659 GQPDHPNVVHLEGVYTKSTPVMIIIFEMENGSLDSFLRQNDGQFTYIQLVGMKRGIAAGM 718  
QY 735 KYLADNMVYHRDLAARNILVNSLVCKVSDFGLSRFLBEDTSDPTTYTSLGSKIPRTWA 794  
Db 719 KYLADNMVYHRDLAARNILVNSLVCKVSDFGLSRFLBEDTSDPTTYTSLGSKIPRTWA 778  
QY 795 PEALQYRKFTSASDVMSYGIIVMVEVNSYGERPYWDMTNDVINAIEQDYRLPPEMCPBA 854  
Db 779 PEALQYRKFTSASDVMSYGIIVMVEVNSYGERPYWDMTNDVINAIEQDYRLPPEMCPBA 838  
QY 855 LHQMLDQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRTTIDYTS 914  
Db 839 LHQMLDQKXNRHPRKFGQIVNTLDKXIRPNLSIKAMAPLSSGINLPLDRTTIDYTS 898  
QY 915 FNTVDEWLEAIKMGQYKESFANAGFTSPDYVSQMMMEDILRLGVTLAAGHKKIINSIQVM 974  
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSPDYVSQMMMEDILRLGVTLAAGHKKIINSIQVM 958  
QY 975 RAQMNQIOSVEV 986  
Db 959 RAQMNQIOSVEV 970

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RESULT 3
US-08-702-367A-11
; Sequence 11, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-11

Query Match      98.2%; Score 5093; DB 2; Length 970;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 15 LLAAYETIMDSRTTAETAEIGMMVHPSPGMEVSGYDENMNTTTRTQVCNVFSSQNMNLR 74
DB 1 LLAAYETIMDSRTTAETAEIGMMVHPSPGMEVSGYDENMNTTTRTQVCNVFSSQNMNLR 60
QY 75 TFFIRRGARHRIHVEKPFVSRDCCSIPSVPGSCKETFNLYYEADFDATKTFFPMWENP 134
DB 61 TFFIRRGARHRIHVEKPFVSRDCCSIPSVPGSCKETFNLYYEADFDATKTFFPMWENP 120
QY 135 WKVVDITLADDESQVLDLGRVWKINTEVRSFGPVRSGFYAFQDYGCMSLIVRVFY 194
DB 121 WKVVDITLADDESQVLDLGRVWKINTEVRSFGPVRSGFYAFQDYGCMSLIVRVFY 180
QY 195 RKCPRITIGALFQETLSGAESTSLVAARGSCIANAEVDVETIKLYCNGDGMVLPIGRG 254
DB 181 RKCPRITIGALFQETLSGAESTSLVAARGSCIANAEVDVETIKLYCNGDGMVLPIGRG 240
QY 255 MCKAGEAVENGTVCGCGPSGTFTKANQGPDACTHCHINSRTTSEGATNCVANGNYIRADL 314
DB 241 MCKAGEAVENGTVCGCGPSGTFTKANQGPDACTHCHINSRTTSEGATNCVANGNYIRADL 300
QY 315 DPLDMCTTTPSPAPQVIVSVNVTSLMLBMTPPRDSGSGEDLVYNIICKSGSGGACTR 374
DB 301 DPLDMCTTTPSPAPQVIVSVNVTSLMLBMTPPRDSGSGEDLVYNIICKSGSGGACTR 360
QY 375 CGDNVQYAPRQGLTEPRRIYISDLAHQYTFEIQAVNGVTDOSPSPFASVNTTNOA 434
DB 361 CGDNVQYAPRQGLTEPRRIYISDLAHQYTFEIQAVNGVTDOSPSPFASVNTTNOA 420
QY 435 APSAVSIMOVSRIVTSITLWSQPOPGVILDYELQYKELSEYNATAIKSPNTVT 494
DB 421 APSAVSIMOVSRIVTSITLWSQPOPGVILDYELQYKELSEYNATAIKSPNTVT 480

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QY 495 VQGLKAGATVYEQVARTVAGYGRYSCKYFQMTAEAYQTSIQEKLPLIISSAAGLVF 554
DB 481 --GLKAGATVYEQVARTVAGYGRYSCKYFQMTAEAYQTSIQEKLPLIISSAAGLVF 538
QY 555 LIAVVTIAIVCNRRGGERADSEYTDLQHTYSGHMPGKIYIDPPTYEDPNEAREFAK 614
DB 539 LIAVVTIAIVCNRRGGERADSEYTDLQHTYSGHMPGKIYIDPPTYEDPNEAREFAK 598
QY 615 EIDISCVKIEQVYAGAFEGEVCSGHLKLPKKEIFVAIKTLKSGYTEKORPFLSEASIM 674
DB 599 EIDISCVKIEQVYAGAFEGEVCSGHLKLPKKEIFVAIKTLKSGYTEKORPFLSEASIM 658
QY 675 GQFDHENVILHEGVYKSTPVMITTEFMENGLSDSLRQNDQFTYIQVGMIRGIAAG 734
DB 659 GQFDHENVILHEGVYKSTPVMITTEFMENGLSDSLRQNDQFTYIQVGMIRGIAAG 718
QY 735 KYLADNMVYHRLAARNILVNSLVCKVSDPGLSRFLEDOTSDPTYSAAGKIPYRMWA 794
DB 719 KYLADNMVYHRLAARNILVNSLVCKVSDPGLSRFLEDOTSDPTYSAAGKIPYRMWA 778
QY 795 PEAIOYRKFTSASDVMSYGIVMWEVMSYGERPYWMTNODVINAIEQYRLPPEMDCPSA 854
DB 779 PEAIOYRKFTSASDVMSYGIVMWEVMSYGERPYWMTNODVINAIEQYRLPPEMDCPSA 838
QY 855 LHQLMDCQKXDRNHRPKFGQIVNTLDKMTIRNNSIKAMAPLSSGINLPILDRITPDYS 914
DB 839 LHQLMDCQKXDRNHRPKFGQIVNTLDKMTIRNNSIKAMAPLSSGINLPILDRITPDYS 898
QY 915 FNTVDEWLEAIKNGQYKESFANAGFTSFVVSQMMEDILRVGVTLAGHOKILNSIQVM 974
DB 899 FNTVDEWLEAIKNGQYKESFANAGFTSFVVSQMMEDILRVGVTLAGHOKILNSIQVM 958
QY 975 RAQNMCIQSVEV 986
DB 959 RAQNMCIQSVEV 970

RESULT 4
PCT-US95-04681-11
; Sequence 11, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04681
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-04681-11

Query Match      98.2%; Score 5093; DB 5; Length 970;

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Best Local Similarity 99.5%; Pred. No. 0;			
Matches 967; Conservative 2; Mismatches 1; Indels 2; Gaps 1;			
QY	15	LLAAVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYOVNVPESQNMWR	74
Db	1	LLAAVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYOVNVPESQNMWR	60
QY	75	TKFRRRGARRIHEVEMKFSVDCSSIPVSGCKETFNLYYYEADPDSATKTFPMNENP	134
Db	61	TKFRRRGARRIHEVEMKFSVDCSSIPVSGCKETFNLYYYEADPDSATKTFPMNENP	120
QY	135	WVAVDTIADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFODYGGCWSLIARVRY	194
Db	121	WVAVDTIADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFODYGGCWSLIARVRY	180
QY	195	RKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEMLVPIGR	254
Db	181	RKCPRIIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEMLVPIGR	240
QY	255	MCKAGEAVENGTVCGCPSGTFRKANOGEACTHCHINSRTTSEGAATNCVNGNGYRDL	314
Db	241	MCKAGEAVENGTVCGCPSGTFRKANOGEACTHCHINSRTTSEGAATNCVNGNGYRDL	300
QY	315	DPLDMPTTIPSAPOAVISSVNETSLMLEMTPRDSGREDLVYNIICKSCSGGACTR	374
Db	301	DPLDMPTTIPSAPOAVISSVNETSLMLEMTPRDSGREDLVYNIICKSCSGGACTR	360
QY	375	CGDNVYAPROLGTEPRRIYISDLAHTQYPELQAVNGVTQSPSPSPASVNTTQA	434
Db	361	CGDNVYAPROLGTEPRRIYISDLAHTQYPELQAVNGVTQSPSPSPASVNTTQA	420
QY	435	APSAVSIHQVSRVDSITLSWSQDPQNGVILDELYEYKELESEYNATAIKSPNTVT	494
Db	421	APSAVSIHQVSRVDSITLSWSQDPQNGVILDELYEYKELESEYNATAIKSPNTVT	480
QY	495	VQGLKAGAIYVQYRARTVAGYGRYSKGYFQTMTEAEVQTSIOEKLPIITSSAAGLV	554
Db	481	--GLKAGAIYVQYRARTVAGYGRYSKGYFQTMTEAEVQTSIOEKLPIITSSAAGLV	538
QY	555	LIAVVAIAIVCNRRGERADSEYTDLOHYTSGHMTGPKKIYIDFETVEDPNEAVREFAK	614
Db	539	LIAVVAIAIVCNRRGERADSEYTDLOHYTSGHMTGPKKIYIDFETVEDPNEAVREFAK	598
QY	615	EIDISCVKIEOYIAGGEFGEVCSGHLKJPGKREIFVALIKLSGYTEKQORDFLSEASIM	674
Db	599	EIDISCVKIEOYIAGGEFGEVCSGHLKJPGKREIFVALIKLSGYTEKQORDFLSEASIM	658
QY	675	GOFDHPNVIHLEGVYTKSTPVMIIITEPMENGLDSFLRONDOGFVILQVGLRGIAAGM	734
Db	659	GOFDHPNVIHLEGVYTKSTPVMIIITEPMENGLDSFLRONDOGFVILQVGLRGIAAGM	718
QY	735	KYLADNMYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPYTSALGKIPIRWTA	794
Db	719	KYLADNMYHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPYTSALGKIPIRWTA	778
QY	795	PEAIDYRKFTSADVWSYGIWMEVMSYGERPYMNTQOVINAIEOYRILPRPNDGCSA	854
Db	779	PEAIDYRKFTSADVWSYGIWMEVMSYGERPYMNTQOVINAIEOYRILPRPNDGCSA	838
QY	855	LHQMLDQKQXRNRPKFGQIVNTLDKIRNPNSLKAMAPLSSGINLPILDRITPYTS	914
Db	839	LHQMLDQKQXRNRPKFGQIVNTLDKIRNPNSLKAMAPLSSGINLPILDRITPYTS	898
QY	915	FNTVEMLEAIKMGYKESFANAGTSFDVVSQMMEDILRLGVTLAGHQKILNSIQVM	974
Db	899	FNTVEMLEAIKMGYKESFANAGTSFDVVSQMMEDILRLGVTLAGHQKILNSIQVM	958
QY	975	RAQNMQIOSVEV 986	
Db	959	RAQNMQIOSVEV 970	

RESULT 5

US-08-162-809-18			
; Sequence 18, Application US/08162809			
; Patent No. 5457048			
; GENERAL INFORMATION:			
; APPLICANT: Pasquale, Elena B.			
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,			
; TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,			
; NUMBER OF SEQUENCES: 26			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: CAMPBELL AND FLORES			
; STREET: 4370 La Tolla Village Drive, Suite 700			
; CITY: San Diego			
; STATE: California			
; COUNTRY: United States of America			
; ZIP: 92122			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/162,809			
; FILING DATE:			
; CLASSIFICATION: 514			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Campbell, Cathryn A.			
; REGISTRATION NUMBER: 31,815			
; REFERENCE/DOCKET NUMBER: P-LJ 9503			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (619) 535-9001			
; TELEFAX: (619) 535-8949			
; INFORMATION FOR SEQ ID NO: 18:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 995 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-162-809-18			
Query Match 96.3%; Score 4993.5; DB 1; Length 995;			
Best Local Similarity 95.8%; Pred. No. 0;			
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;			
QY	10	LLPLPLAAVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYOVNVPESQ	69
Db	18	LLPLPLAAVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYOVNVPESQ	77
QY	70	NNMLRTKTYIRRGARRIHEVEMKFSVDCSSIPVSGCKETFNLYYYEADPDSATKTFPN	129
Db	78	NNMLRTKTYIRRGARRIHEVEMKFSVDCSSIPVSGCKETFNLYYYEADPDSATKTFPN	137
QY	130	MMENPMVKVDTTIADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFODYGGCWSLI	189
Db	138	MMENPMVKVDTTIADESFQVDLGRVVKINTEVRSFGPVRSQGYLAFODYGGCWSLI	197
QY	190	VRFVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEMLV	249
Db	198	VRFVYRKCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGEMLV	257
QY	250	PICRCMKXGFEVENGTVCGCPSGTFRKANOGEACTHCHINSRTTSEGAATNCVNGNY	309
Db	258	PICRCMKXGFEVENGTVCGCPSGTFRKANOGEACTHCHINSRTTSEGAATNCVNGNY	317
QY	310	YRADLPDMPCTTIPSAPOAVISSVNETSLMLEMTPRDSGREDLVYNIICKSCSGGR	369
Db	318	YRADLPDMPCTTIPSAPOAVISSVNETSLMLEMTPRDSGREDLVYNIICKSCSGGR	377
QY	370	GACTRCGDNVQYAPROLGTEPRRIYISDLAHTQYTFELQAVNGVTQSPSPSPASVNI	429
Db	378	GACTRCGDNVQYAPROLGTEPRRIYISDLAHTQYTFELQAVNGVTQSPSPSPASVNI	437
QY	430	TTNOAPSAVSIHQVSRVDSITLSWSQDPQNGVILDELYEYKELESEYNATAIKSP	489

Mon Aug 30 08:48:58 2004

us-09-914-883-2.aug04.ra1

Page 5

Db 438 TTNOAPSAVSIIMHQVSRITVDSITLWSQPODPQNVILLIDYLOYYEKNLSLUNSTAVKSP 497  
 QY 490 TINTVYQGIKAGIAYVQVARTVAGYSGSKMFCOTMBAEYOTSIOEKLPLIISSA 549  
 Db 498 TINTVYQNKAGITVYFQVARTVAGYSGSKMFCOTMBAEYOTSIOEKLPLIISSA 557  
 QY 550 AGVFLIAYVVAIVON -RRGFRADESITDCLQHTSGNTPGMKIYIDPFTYEDNEA 608  
 Db 558 AGVFLIAYVVAIIYVNRFRGERADSEYTDCLQHTSGNTPGMKIYIDPFTYEDNEA 617  
 QY 609 VREFAKEIDISCYKIEQVIGAGBFGVCSGHLKLPKKEIFVAIKTLKSGYTEKORDFL 666  
 Db 618 VREFAKEIDISCYKIEQVIGAGBFGVCSGHLKLPKKEIFVAIKTLKSGYTEKORDFL 677  
 QY 669 SEASINGQDPHPVITHLESVTKSPVMTTEBMEKNSLDSFLQNDQOFTVILVGLMR 728  
 Db 678 SEASINGQDPHPVITHLESVTKSPVMTTEBMEKNSLDSFLQNDQOFTVILVGLMR 737  
 QY 729 GIAGAKKYIADMMYVYRDLAARNILVNSLVOKVSDFLSFLRDLDDSDPTYSALGKI 788  
 Db 738 GIAGAKKYIADMMYVYRDLAARNILVNSLVOKVSDFLSFLRDLDDSDPTYSALGKI 797  
 QY 789 PIRWTAPEAIQYRKFTSASDVWSYGIWMEVNSYGEREYMDMTNODYINAIQDYRLPP 848  
 Db 798 PIRWTAPEAIQYRKFTSASDVWSYGIWMEVNSYGEREYMDMTNODYINAIQDYRLPP 857  
 QY 849 MDCPSALLHQMIDCMQKDXNRHPRKQGVNTLDMKIRNPNLSKAPLSSGNIPLDRT 908  
 Db 858 MDCPSALLHQMIDCMQKDXNRHPRKQGVNTLDMKIRNPNLSKAPLSSGNIPLDRT 917  
 QY 909 IPDYTSFNTVDENLEAIKMGQYKESFANAGFTSPDVWSQMMEDILRLGYTLACHQKIL 968  
 Db 918 IPDYTSFNTVDENLEAIKMGQYKESFANAGFTSPDVWSQMMEDILRLGYTLACHQKIL 977  
 QY 969 NSTQVMEAOQNOQISYEYV 986  
 Db 978 NSTQVMEAOQNOQISYEYV 995  
 RESULT 6  
 US-08-162-809-12  
 Sequence 12, Application US/08162809  
 Patent No. 5457048  
 GENERAL INFORMATION:  
 APPLICANT: Pasquale, Elena B.  
 APPLICANT: Sajjadi, Fereydoon G.  
 TITLE OF INVENTION: NOVEL BPH-RELATED TYROSINE KINASES,  
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAMPBELL AND FLORES  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 City: San Diego  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 92122  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/162,809  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LT 9503  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949

```

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1011 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-162-809-12

Query Match      95.8%; Score 4971.5; DB 1; Length 1011;
Best Local Similarity 94.2%; Pred. No. 0;
Matches 936; Conservative 29; Mismatches 12; Indels 17; Gaps 2

QY      10 LLLPLLAVEETLNDSTTATBELGMMVHPSPGMEEVSYGDEMNTIRTYQVCNVESSQ 69
Db      18 LALLPLLAVEETLNDSTTATBELGMMVHPSPGMEEVSYGDEMNTIRTYQVCNVESSQ 77

QY      70 NNNLRTKPIRRRGARHIVEMKFSYRDCSSIPSYPGSCKETFNLYYYEADFDSATKTFPN 129
Db      78 NNNLRTKPIRRRGARHIVEMKFSYRDCSSIPNVPGSCKETFNLYYYESDFDATKTFPN 137

QY      130 WMENPNVAKDTTAADESPQVDLGRVWKINTIEVRSFGPSRSQFYLAPODYGCGKSLIA 189
Db      138 WMENPNMKADTTAADESPQVDLGRVWKINTIEVRSFGPSKNGFYLAPODYGCGKSLIA 197

QY      190 VRFVYKRCRIIQQNGAIFQETLSGAESTSLVAARGSCIIANAEEVDVYIKLYCNGDGEMLV 249
Db      198 VRFVYKRCRIVQQNGAVFQETLSGAESTSLVAARGTCSINAEEVDVYIKLYCNGDGEMLV 257

QY      250 PIRCRCKAGFEAVENGTYCRCGPGGTAKAQQGSDACTHCPINSRTTSEATNVCVRNG 309
Db      258 PIRCRCKRGYSVENVGVCRGCPGTAKAQGGGCVHCPINSRTTSEATNVCVRNG 317

QY      310 YRADLPLMPCTTIPSAQAVISVNETSLMLETTPPDGSGREDLVYNIICKSGSGR 369
Db      318 YRADADPVMPTCTTIPSAQAVISVNETSLMLETTPPDGSGREDLVYNIICKSGSGR 377

QY      370 GACTRCGDNVQAPRQOLGTEBRIYISDLAHTQYTEIQAVNGVTDQSPFSQFASVNI 429
Db      378 GACTRCGDNVQAPRQOLGTEBRIYISDLAHTQYTEIQAVNGVTDQSPFSQFASVNI 437

QY      430 TTNQAPASVSIIMHOVSRTVDSITLSWQPOCPQGVLLDVELQYKEKLESEVATLTKSF 489
Db      438 TTNQAPASVSIIMHOVSRTVDSITLSWQPOCPQGVLLDVELQYKEKLESEVATLTKSP 497

QY      490 TINTVYQGLKAGAIYVFQVRAATVAGYGRYSKMYFQTMTEAEVQTSIQEKLPILIGSSA 549
Db      498 TINTVYQGLKAGHIVYFQVRAATVAGYGRYSKMYFQTMTEAEVQTSIQEKLPILIGSSA 557

QY      550 AGVFLILAVVLAIVCN-RRGFERADSYTKLQHTYSGH-----MTPG 592
Db      558 AGVFLILAVVLAIVCNRRRGFERADSYTKLQHTYSGHSTRGPPGLGVASLPVTPG 617

QY      593 MKIYIDPFYEDPNEAVVEFAKEIDISCVKLEQVIGAGEFEVCSGHLKPGREILFVAL 652
Db      618 MKIYIDPFYEDPNEAVVEFAKEIDISCVKLEQVIGAGEFEVCSGHLKPGREILFVAL 677

QY      653 KTLKSGTYSKQRRDPSSEASIMGQDHNVYHLEGVYTKSPVMIITEFENSGSLDSFLR 712
Db      678 KTLKSGTYSKQRRDPSSEASIMGQDHNVYHLEGVYTKSPVMIITEFENSGSLDSFLR 737

QY      713 QNDGQFTVQLVGMIRGLAAGMKYIADNNVYHRDLAARNILVANSNLYCAKSDGSLRSFLE 772
Db      738 QNDGQFTVQLVGMIRGLAAGMKYIADNNVYHRDLAARNILVANSNLYCAKSDGSLRSFLE 797

QY      773 DDTSDPTTYSALGKIPIRWTAPEAIQYRKTTASDVWSYIGIVYMEVMSYGEFPIYMDTN 832
Db      798 DDTSDPTTYSALGKIPIRWTAPEAIQYRKTTASDVWSYIGIVYMEVMSYGEFPIYMDTN 857

QY      833 QDVYNALIEDYRLPEPMQCPNALHQLMLDQCQXRNNRPFGQIVNTLDKINPNLSLKA 892
Db      858 QDVYNALIEDYRLPEPMQCPNALHQLMLDQCQXRNNRPFGQIVNTLDKINPNLSLKA 917

QY      893 MADSISGINLPLIDRTIPDYTSFNTVDWMLFAIKMGQYKESFANAGTSPDVVSQVMMED 952

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Db 918 MAELSSGVNPLDRLTPTDTSFNTVDENMLDAIKMSQYKESFASAGFTTFDVSQMTVED 977  
Qy 953 ILRLGVTLAGHCKILINSIQVMAQNMQIOSVEV 986  
Db 978 ILRVGVTLAGHCKILINSIQVMAQNMQIOSVEV 1011

## RESULT 7

US-08-673-789-5  
Sequence 5, Application US/08673789  
Patent No. 5814479  
GENERAL INFORMATION:  
APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,  
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,  
APPLICANT: GEORGE, F.  
TITLE OF INVENTION: BSK RECEPTOR LIKE  
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR  
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/673,789  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/177,812  
FILING DATE: 04-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPEI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ. ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 995  
TYPE: AMINO ACID  
STRANDEDNESS: UNKNOWN  
TOPOLOGY: UNKNOWN  
US-08-673-789-5

Query Match 95.7%, Score 4962.5, DB 2, Length 995,  
Best Local Similarity 95.1%, Pred. No. 0,  
Matches 930, Conservative 30, Mismatches 17, Indels 1, Gaps 1,  
Qy 10 LLLPLLAAVEETLMDSTATAELGWMVHPPSGWEVSGYDENMNTIRTYQYCNVFESSQ 69  
Db 18 LALLPLLAAVEETLMDSTATAELGWMVHPPSGWEVSGYDENMNTIRTYQYCNVFESSQ 77  
Qy 70 NNMWLRFTKFIIRRGARHIVHEMKFSVVDGSLPSVPSGCKETNLYYYEADPFSATKTFPN 129  
Db 78 NNMWLRFTKFIIRRGARHIVHEMKFSVVDGSLPSVPSGCKETNLYYYEADPFSATKTFPN 137  
Qy 130 WKENPVMKVDITLAADSGFQVDLGGVWVKINTEVRSFGVSRSGFYLAFODYGGGMSLIIA 189  
Db 138 WKENPVMKVDITLAADSGFQVDLGGVWVKINTEVRSFGVSRSGFYLAFODYGGGMSLIIA 197  
Qy 190 VRVFYKCPRIIIONGAIFOETLSGAESTSLVAARSSCIANAEEVDVPIKLYCNGDGEWLV 249

Db 198 VRVFYKCPRIIIONGAIFOETLSGAESTSLVAARSSCIANAEEVDVPIKLYCNGDGEWLV 257  
Qy 250 PIGRCWKAGEAVENGTVRCGCPSGTFKANOGDEACTHCPINSRTISEGATNCVCRNGY 309  
Db 258 PIGRCWKAGEAVENGTVRCGCPSGTFKANOGDEACTHCPINSRTISEGATNCVCRNGY 317  
Qy 310 YRADLPDLMPCCTTIPAPAVISSVNETSLMELMTPRDSGGRDLVYNIICKSGSGR 369  
Db 318 YRADLPDLMPCCTTIPAPAVISSVNETSLMELMTPRDSGGRDLVYNIICKSGSGR 377  
Qy 370 GACTRCGDNDVQAPRQJLGEPRYIYISDLAHTQYFEIQAQVAVTDDSPFSQFASVNI 429  
Db 378 GACTRCGDNDVQAPRQJLGEPRYIYISDLAHTQYFEIQAQVAVTDDSPFSQFASVNI 437  
Qy 430 TTNOAASAVSINHQSRTVDSITLSNSQPDQNGVILDELOYEKESEYNATAIKSP 489  
Db 438 TTNOAASAVSINHQSRTVDSITLSNSQPDQNGVILDELOYEKESEYNATAIKSP 497  
Qy 490 TINTVVOGLKAGAIYVQVARTVAGYGRYSGKVFQIMTEAEYQTSIGCKPLIIGSSA 549  
Db 498 TINTVVOGLKAGAIYVQVARTVAGYGRYSGKVFQIMTEAEYQTSIGCKPLIIGSSA 557  
Qy 550 AGLVFLIAVVIAIVCN-RGFERADSEYTDKLQHTSGHMPQMKIYIDPFYEDPNEA 608  
Db 558 AGLVFLIAVVIAIVCN-RGFERADSEYTDKLQHTSGHMPQMKIYIDPFYEDPNEA 617  
Qy 609 VREFAKEDISCVKIEBQVIGAGEFEGVCSGHLKLPGRREIFVAIKTLKSGYTEKQSRDFI 668  
Db 618 VREFAKEDISCVKIEBQVIGAGEFEGVCSGHLKLPGRREIFVAIKTLKSGYTEKQSRDFI 677  
Qy 669 SEASIMQFDPHPVNIHLEGVYTKSTPWIITTEPMENGSLDSFLRQNDQGFVIQIVGMUR 728  
Db 678 SEASIMQFDPHPVNIHLEGVYTKSTPWIITTEPMENGSLDSFLRQNDQGFVIQIVGMUR 737  
Qy 729 GIAQMKYLDMMYVHBDLAARNLIVNSNVCVSPFGLSRFLEDTPSPTYSAIGKI 788  
Db 738 GIAQMKYLDMMYVHBDLAARNLIVNSNVCVSPFGLSRFLEDTPSPTYSAIGKI 797  
Qy 789 PIRWTAPEALQYRKFTSASDWSYGIWMEVMSYGERPYWDMTNOQVINAIEQDYRLPP 848  
Db 798 PIRWTAPEALQYRKFTSASDWSYGIWMEVMSYGERPYWDMTNOQVINAIEQDYRLPP 857  
Qy 849 MDCPSALHQLMDCWQDRVHRPKFGQIVNTLDKMTNRPUSLKAMPPLSSGINTLPLDRT 908  
Db 858 MDCPSALHQLMDCWQDRVHRPKFGQIVNTLDKMTNRPUSLKAMPPLSSGINTLPLDRT 917  
Qy 909 IPDYSFNTVDENMLDAIKMSQYKESFASAGFTTFDVSQMTVEDILRVGVTLAGHCKIL 968  
Db 918 IPDYSFNTVDENMLDAIKMSQYKESFASAGFTTFDVSQMTVEDILRVGVTLAGHCKIL 977  
Qy 969 NSIQVMAQNMQIOSVEV 986  
Db 978 NSIQVMAQNMQIOSVEV 995

Search completed: August 28, 2004, 04:15:00  
Job time : 26.1886 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:08:55 ; Search time 62.8025 Seconds  
(without alignments)  
4939.422 Million cell updates/sec

Title: US-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MALRRIGALLLLPLLAWE.....INSIQVRAQWNCIQSEV 986

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_NEW\_PUB.pep.\*
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  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5181	99.9	1055	US-10-648-593-139	Sequence 139, App
2	5171.5	99.7	987	US-10-295-027-1193	Sequence 1193, Ap
3	4993.5	99.5	12	US-10-029-020-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1  
US-10-648-593-139  
; Sequence 139, Application US/10648593  
; Publication No. US20040106132A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT

TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
FILE REFERENCE: D0273 NP  
CURRENT APPLICATION NUMBER: US/10/648-593  
CURRENT FILING DATE: 2003-08-26  
PRIOR APPLICATION NUMBER: 60/406,385  
PRIOR FILING DATE: 2002-08-27  
NUMBER OF SEQ ID NOS: 557  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 139  
LENGTH: 1055  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-648-593-139

Query Match 99.9% Score 5181; DB 16; Length 1055;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRRIGALLLLPLLAWEETLMDSTTATAGMTYHPSGWEVSGYDENMTTIRYQ	60
DB	1	MALRRIGALLLLPLLAWEETLMDSTTATAGMTYHPSGWEVSGYDENMTTIRYQ	60
QY	61	VCNPFESSQNNWLTKTIRRGARHRYENKFSYDCCSIPSVGSCKEFTNLYYEADF	120
DB	61	VCNPFESSQNNWLTKTIRRGARHRYENKFSYDCCSIPSVGSCKEFTNLYYEADF	120
QY	121	DSATKTFPMNMENWVVDITAADESFOYDLGGRVAKINTEVSPFVSASGTYLAFOD	180
DB	121	DSATKTFPMNMENWVVDITAADESFOYDLGGRVAKINTEVSPFVSASGTYLAFOD	180
QY	181	YGGCMSLIAVRFYRKCPRITIOGAIFQETLSGAESTSLVAARSCIAAEVDVPIKLY	240
DB	181	YGGCMSLIAVRFYRKCPRITIOGAIFQETLSGAESTSLVAARSCIAAEVDVPIKLY	240
QY	241	CNGGEMLVPIGRCMCAFEAVENGTCVCGPGSTKANOGDCAHCPINSTTSEGA	300
DB	241	CNGGEMLVPIGRCMCAFEAVENGTCVCGPGSTKANOGDCAHCPINSTTSEGA	300
QY	301	TNCVCRNGYRADLPDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLYNI	360
DB	301	TNCVCRNGYRADLPDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLYNI	360
QY	361	ICKCGSGRGACRCCGNVQYAPQGLTEPRITISLLAHOTYTFEIOAVNGYTDSPF	420
DB	361	ICKCGSGRGACRCCGNVQYAPQGLTEPRITISLLAHOTYTFEIOAVNGYTDSPF	420
QY	421	SPQASVNTITNQAFAVSIHMOVSRTVDSITLSWQPOQPNVILDEYLOVEKELSE	480
DB	421	SPQASVNTITNQAFAVSIHMOVSRTVDSITLSWQPOQPNVILDEYLOVEKELSE	480
QY	481	YNATPAIKSPNTVTVOGLKAGAIYFOVAPRTVAGYGRYSGKWFQMTDAEYOTSIOEK	540
DB	481	YNATPAIKSPNTVTVOGLKAGAIYFOVAPRTVAGYGRYSGKWFQMTDAEYOTSIOEK	540
QY	541	LPLTIGSSAAGLVLLIAVVIATVCNRRGEPADSEYTDLOHTSGHMTPKMKIYIDPF	600
DB	541	LPLTIGSSAAGLVLLIAVVIATVCNRRGEPADSEYTDLOHTSGHMTPKMKIYIDPF	600
QY	601	TYEDPNEAVRFAKEIDISCVKIEQVIGAGEFEGVCSGHLKPKREI FVAIKTLKSGYT	660
DB	601	TYEDPNEAVRFAKEIDISCVKIEQVIGAGEFEGVCSGHLKPKREI FVAIKTLKSGYT	660
QY	661	EKQARDLSASITMGCDHPNVTHLGGVTKSPVMTTEPMNGSIDSLRQNDQGFYV	720
DB	661	EKQARDLSASITMGCDHPNVTHLGGVTKSPVMTTEPMNGSIDSLRQNDQGFYV	720
QY	721	IQLVGMRLGIAAGKYLADNNVYHRDLAAENILVNSNLVCKVSDFGLSRFLDDTSPTY	780
DB	721	IQLVGMRLGIAAGKYLADNNVYHRDLAAENILVNSNLVCKVSDFGLSRFLDDTSPTY	780
QY	781	TSALGGLPIPRWAPPAIYQRRKTSASDWVSXGIVMKEWVSXGEPFVMDTNDQVNAIE	840

Db 781 TSALGKIPRWTAPBAIQYRKFTSADVWSYGI VMMWEVMSYGERPYMDNTQDVINAIE 840  
 QY 841 QDRLEPPMDCCPSALHQLMDCWQKDRNRHPRFGQIVNTLDKXIRNPNLSLKMAPLSSGI 900  
 Db 841 QDRLEPPMDCCPSALHQLMDCWQKDRNRHPRFGQIVNTLDKXIRNPNLSLKMAPLSSGI 900  
 QY 901 INFLDRLTIPDYTSFNTVDWMLFAIKMGQYKESFANAGFTSPDVVSQMMMEDILRLGYTL 960  
 Db 901 INFLDRLTIPDYTSFNTVDWMLFAIKMGQYKESFANAGFTSPDVVSQMMMEDILRLGYTL 960  
 QY 961 AGHQKILINSIQYMRQAQNOIQSVE 985  
 Db 961 AGHQKILINSIQYMRQAQNOIQSVE 985

RESULT 2  
 US-10-295-027-1193  
 ; Sequence 1193, Application US/10295027  
 ; Publication No. US200302350A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Afari, Daniel  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Ginsberg, Wendy M.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Glynn, Richard  
 ; APPLICANT: Hevezal, Peter A.  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Watson, Susan R.  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and  
 ; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer  
 ; FILE REFERENCE: 018501-012500US  
 ; CURRENT APPLICATION NUMBER: US/10/295, 027  
 ; CURRENT FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: US 09/663, 733  
 ; PRIOR FILING DATE: 2000-09-15  
 ; PRIOR APPLICATION NUMBER: US 60/350, 666  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/335, 394  
 ; PRIOR FILING DATE: 2001-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/332, 464  
 ; PRIOR FILING DATE: 2001-11-21  
 ; PRIOR APPLICATION NUMBER: US 60/334, 393  
 ; PRIOR FILING DATE: 2001-11-29  
 ; PRIOR APPLICATION NUMBER: US 60/340, 376  
 ; PRIOR FILING DATE: 2001-12-14  
 ; PRIOR APPLICATION NUMBER: US 60/347, 211  
 ; PRIOR FILING DATE: 2002-01-08  
 ; PRIOR APPLICATION NUMBER: US 60/347, 349  
 ; PRIOR FILING DATE: 2002-01-10  
 ; PRIOR APPLICATION NUMBER: US 60/355, 250  
 ; PRIOR FILING DATE: 2002-02-08  
 ; PRIOR APPLICATION NUMBER: US 60/356, 714  
 ; PRIOR FILING DATE: 2002-02-13  
 ; Remaining prior Application data removed - See file wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 1386  
 ; SOFTWARE: Patentln Ver. 2.1  
 ; SEQ ID NO 1193  
 ; LENGTH: 987  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-295-027-1193

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RESULT 3  
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 ; Sequence 62, Application US/10029020  
 ; Publication No. US2004003971A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gangoli et al.  
 ; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-225  
 ; CURRENT APPLICATION NUMBER: US/10/029, 020



/ CURRENT FILING DATE: 2001-12-19  
 / PRIOR APPLICATION NUMBER: 60/256,704  
 / PRIOR FILING DATE: 2000-12-19  
 / PRIOR APPLICATION NUMBER: 60/311,590  
 / PRIOR FILING DATE: 2001-08-10  
 / PRIOR APPLICATION NUMBER: 60/257,314  
 / PRIOR FILING DATE: 2000-12-20  
 / PRIOR APPLICATION NUMBER: 60/311,613  
 / PRIOR FILING DATE: 2001-08-10  
 / PRIOR APPLICATION NUMBER: 60/315,617  
 / PRIOR FILING DATE: 2001-08-29  
 / PRIOR APPLICATION NUMBER: 60/307,506  
 / PRIOR FILING DATE: 2001-07-24  
 / PRIOR APPLICATION NUMBER: 60/322,358  
 / PRIOR FILING DATE: 2001-09-14  
 / PRIOR APPLICATION NUMBER: 60/294,075  
 / PRIOR FILING DATE: 2001-05-29  
 / PRIOR APPLICATION NUMBER: 60/288,153  
 / PRIOR FILING DATE: 2001-05-02  
 / NUMBER OF SEQ ID NOS: 190  
 / SOFTWARE: PatentIn Ver. 2.1  
 / SEQ ID NO: 62  
 / LENGTH: 995  
 / TYPE: PR  
 / ORGANISM: Gallus gallus  
 US-10-029-020-62

Query Match 96.3%; Score 4993.5; DB 12; Length 995;  
 Best Local Similarity 95.8%; Pred. No. 0;  
 Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

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 DB 78 NMLRTRKFIIRRGARHIEHMKSVSDCSIPSPSCKETRLYYEADPDSATKTFPN 137  
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 DB 138 WKENPMKVDITLADSFQVDLGRVMKINTEVRSFGVPSRSGFYLAFOYGGCWSLIA 197  
 QY 190 VRFVYKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPILYCNCGDEWLV 249  
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 QY 310 YRADLPDLMPCCTTIPSAPOAVISSVNETSLMLEWTTPRDSGREDLVYNIICKSGSGR 369  
 DB 318 YRADLPDLMPCCTTIPSAPOAVISSVNETSLMLEWTTPRDSGREDLVYNIICKSGSGR 377  
 QY 370 GACTRCGDNVQYAPROGLTEPRYISDLAHOYFEEIOAVNGVTDOSPPSPQFASVNI 429  
 DB 378 GACTRCGDNVQYAPROGLTEPRYISDLAHOYFEEIOAVNGVTDOSPPSPQFASVNI 437  
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 DB 438 TTNQAPSAVSIMHQSRTVDSITLSMSQPDQPNVILIDYELQYKEKLESEYNATAIKSP 497  
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 QY 550 AGIVFLIAVVVIAVGN-RRGFRADESEYDKLQHTSGHMTPGMKIYIDPFYEDPNEA 608  
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 Job time : 63.8025 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:54 ; Search time 19.3577 Seconds  
(without alignments)  
2796.715 Million cell updates/sec

Title: US-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MALRRLGALLPLLAIVE.....LINSIQVRAQWQIQSYEV 986

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB	ID Description
1	5184	99.9	1055 1 EPH2 HUMAN P29323 homo sapien
2	5130	98.9	994 1 EPH2 MOUSE P54763 mus musculu
3	4975.5	95.9	1004 1 EPH2 CHICK P28693 gallus gall
4	4945	95.3	987 1 EPH2 COTUJA Q90344 coturnix co

#### ALIGNMENTS

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EPH2\_HUMAN STANDARD; PRT; 1055 AA.  
ID EPH2\_HUMAN  
AC P29323; O43477;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.113) (Tyrosine-protein kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HK5) (BRK).  
GN EPHB2 OR EPH3 OR ERK OR DRT OR HEK5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Fetal brain;  
RX MEDLINE=66154673; PubMed=8589679;  
RA Ikegaki N., Tang X.X., Liu X.-G., Siegel J.A., Allen C., Yoshioaka A., Sultan E.P., Brodeur G.M., Pleasure D.B.;  
RT "Molecular characterization and chromosomal localization of DRT (EPH3): a developmentally regulated human protein-tyrosine kinase gene of the EPH family.";

RL Hum. Mol. Genet. 4:2033-2045(1995).  
RC [2]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Gastric carcinoma;  
RX MEDLINE=93343925; PubMed=7688222;  
RA Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;  
RT "Identification of protein-tyrosine kinase genes preferentially expressed in embryo stomach and gastric cancer.";  
RL Biochem. Biophys. Res. Commun. 194:698-705(1993).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RC TISSUE=Fetal brain;  
RX MEDLINE=98359217; PubMed=9696046;  
RA Tang X.X., Pleasure D.B., Brodeur G.M., Ikegaki N.;  
RT "A variant transcript encoding an isoform of the human protein tyrosine kinase EPHB2 is generated by alternative splicing and alternative use of polyadenylation signals.";  
RL Oncogene 17:521-526(1998).  
RN [4]  
RP SEQUENCE OF 15-986 FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Brain;  
RX MEDLINE=95206782; PubMed=7898931;  
RA Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M., Basu R., Welcher A.A.;  
RT "cDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";  
RL Oncogene 10:897-905(1995).  
RN [5]  
RP SEQUENCE OF 509-986 FROM N.A. (ISOFORM SHORT).  
RC TISSUE=Brain;  
RX Saito T., Maehiko S., Kitahara M., Murata M., Yamamoto Y., Hori T., Matsuda Y.;  
RT Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 652-712 FROM N.A.  
RX MEDLINE=91296384; PubMed=1648701;  
RA Chan J., Watt V.M.;  
RT "eek and erk, new members of the eph subclass of receptor protein-tyrosine kinases.";  
RL Oncogene 6:1057-1061(1991).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (ISOFORM SHORT).  
RX MEDLINE=99132419; PubMed=9933164;  
RA Thanoos C.D., Goodwill K.E., Bowie J.U.;  
RT "Oligomeric structure of the human EphB2 receptor SAM domain.";  
RL Science 283:833-836(1999).  
CC -1- FUNCTION: Receptor for members of the ephrin-B family.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
CC -1- SUBUNIT: The ligand-activated form interacts with multiple proteins, including GRASP-activating protein (RASGAP) through its SH2 domain. Binds RASGAP through the juxtamembrane tyrosines residues. Interacts with PRKCAP (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long; Synonyms=EPHB2V;  
CC IsoId=P29323-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P29323-2; Sequence=VSP\_003016, VSP\_003017;  
CC -1- TISSUE SPECIFICITY: Brain, heart, lung, kidney, placenta, pancreas, liver and skeletal muscle. Preferentially expressed in fetal brain.  
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

Query Match	Best Local Similarity	99.9% Score	5184; DB 1; Length	1055;
Matches	985; Conservative	0; Mismatches	0; Indels	0; Gaps
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FT VARSPLIC	987	1055	/FTID=VSP_003016.	
FT VARSPLIC	987	1055	Missing (in isoform Short).	
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FT VARIANT	671	671	MALRGLGALLLLPLLAAVE -> MWVPLALPVCTYA	
FT CONFLICT	1	20	(in REF. 2).	
FT CONFLICT	154	154	G -> D (in REF. 2).	
FT CONFLICT	476	476	K -> KQ (in REF. 2).	
FT CONFLICT	495	496	MISSING (in REF. 4).	
FT CONFLICT	532	532	E -> D (in REF. 2).	
FT CONFLICT	568	568	R -> RR (in REF. 1).	
FT CONFLICT	589	589	M -> I (in REF. 4).	
FT CONFLICT	788	788	I -> F (in REF. 4).	
FT CONFLICT	853	853	S -> A (in REF. 2 AND 5).	
FT CONFLICT	923	923	E -> K (in REF. 2 AND 5).	
FT CONFLICT	956	956	L -> V (in REF. 3).	
FT CONFLICT	958	958	V -> L (in REF. 1).	
FT HELIX	918	924		
FT TURN	925	926		
FT HELIX	928	930		
FT HELIX	931	936		
FT TURN	937	938		
FT HELIX	942	945		
FT TURN	946	947		
FT HELIX	950	956		
FT TURN	957	957		
FT HELIX	961	984		
SEQUENCE	1055 AA;	117506 MM;	D0AA2CC8EE6CDBC8 CRC64;	

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QY 601 TYDDENAVNREFPKEDIDISCVKLEQYITGAGEFGEVSGHLKLPGRKEITVAIKTKSGYT 660
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DB 841 QDYRLPPMDCPBALHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPSLKAAPLSSGI 900
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DB 961 AGHQKILINSIQVRAQNMQIOGVE 985

RESULT 2
EPB2 MOUSE STANDARD; PRT; 994 AA.
ID EPB2 MOUSE STANDARD; PRT; 994 AA.
AC P54763; Q62213; Q9QVY4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor Eph-3) (Neural kinase) (Nuk receptor tyrosine kinase) (SEK-3).
GN EPB2 OR EPB3 OR NUK OR SEK3.
OS Mus musculus (Mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9418250; PubMed=8134103;
RA Henkemeyer M., Marengere L.E., McGlade J., Olivier J.P., Conlon R.A., Holmward D.P., Letwin K., Pawson T.,
RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles in segmental patterning of the brain and axonogenesis.",
RL Oncogene 9:1001-1014(1994).
RN [2]
RP SEQUENCE OF 516-994 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=95034306; PubMed=7947319;
RA Becker N., Seltanidou T., Murphy P., Mattei M.-G., Topilko P., Nieto A., Wilkinson D.G., Charnay P., Gialardi P.,
RT "Several receptor tyrosine kinase genes of the Eph family are segmentally expressed in the developing hindbrain.",
RL Mech. Dev. 47:3-17(1994).
RN [3]
RP FUNCTION
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.,
RT "Complementary expression of transmembrane ephrins and their receptors in the mouse spinal cord: a possible role in constraining the RT orientation of longitudinally projecting axons.",
RL Development 127:1397-1410(2000).

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RN [4]
RP INTERACTION WITH PRKCAP.
RX MEDLINE=99098206; PubMed=9883737;
RA Torres R., Firestein B.L., Dong H., Staudinger J., Olson E.N., Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.,
RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph receptors and their ephrin ligands.",
RL Neuron 21:1453-1463(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 29-204.
RX MEDLINE=99066648; PubMed=9853759;
RA Himanen J.-P., Henkemeyer M., Nikolov D.B.,
RT "Crystal structure of the ligand-binding domain of the receptor tyrosine kinase EphB2.",
RL Nature 396:486-491(1998).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 29-208 IN COMPLEX WITH EPHRIN-B2.
RX MEDLINE=21638766; PubMed=11780069;
RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A., Henkemeyer M., Nikolov D.B.,
RT "Crystal structure of an Eph receptor-ephrin complex.",
RL Nature 414:933-938(2001).
CC -1- FUNCTION: Receptor for members of the ephrin-B family. Can function in aspects of retinal ganglion cell axon guidance to the optic disk even lacking its tyrosine kinase domain.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCAP. The ligand-activated form interacts with multiple proteins, including GTPase-activating protein (RASGAP) through its SH2 domain. Binds RASGAP through the juxtamembrane tyrosine residues. Interacts with PRKCAP (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in cells of the developing outer retina.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.
CC -----
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CC -----
DR EMBL, L25890; AAA72411.1; ALT_INIT.
DR EMBL, X76011; CAAS3598.1; -.
DR PDB, 1KGY; 28-MAY-02.
DR PDB, 1NUK; 13-OCT-99.
DR GO; MGI:99611; Ephb2.
DR GO; GO:0008046; F:axon guidance receptor activity; IDA.
DR GO; GO:0007411; P:axon guidance; IDA.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003962; FN_III_subd.
DR InterPro; IPR008979; Gal_bind_1like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; Ykase_receptorov.
DR Pfam; PF01404; EPH_1bd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.

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Prodom; PD001495; Ephrin receptor; 1.  
 DR Prodom; PD000001; Prot kinase; 1.  
 DR SMART; SM000615; Eph\_1b2; 1.  
 DR SMART; SM000660; FN3\_2; 1.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; Tyk2; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS00105; SAM\_DOMAIN; 1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.  
 FT SIGNAL 1 26  
 FT CHAIN 27 994  
 FT DOMAIN 27 551  
 FT TRANSFEM 552 572  
 FT 573 994  
 FT DOMAIN 192 329  
 FT DOMAIN 330 439  
 FT DOMAIN 440 537  
 FT DOMAIN 629 892  
 FT DOMAIN 921 985  
 FT SITE 994 994  
 FT NP\_BIND 635 643  
 FT BINDING 661 661  
 FT ACT\_SITE 754 754  
 FT MOD\_RES 604 604  
 FT MOD\_RES 610 610  
 FT MOD\_RES 788 788  
 FT MOD\_RES 938 938  
 FT DISULFID 70 192  
 FT DISULFID 103 115  
 FT CARBOHYD 273 273  
 FT CARBOHYD 344 344  
 FT CARBOHYD 436 436  
 FT CARBOHYD 490 490  
 FT CONFLICT 576 576  
 SQ SEQUENCE 994 AA; 110759 MW; BCB9B12A070394C CRC64;

Query Match 98.9%; Score 5130; DB 1; Length 994;  
 Best Local Similarity 99.5%; Pred. No. 2,1e-315;  
 Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLAEEETLMSTTATLGMVHPSCGMEVSGYDENMTIRTYOVCNVFESSQ 69  
 DB 18 LLLPLLAEEETLMSTTATLGMVHPSCGMEVSGYDENMTIRTYOVCNVFESSQ 77  
 QY 70 NNMRTKFIIRRGARHLHVMKFSVYDCSIPSPCKETENLYYYEADFPSATKTFPN 129  
 DB 78 NNMRTKFIIRRGARHLHVMKFSVYDCSIPSPCKETENLYYYEADFPSATKTFPN 137  
 QY 130 WMENPWKVDITIADESPSCVDIGRVMKINTEVRSFGPVSRSGFYLAFODYGCMSLIA 189  
 DB 138 WMENPWKVDITIADESPSCVDIGRVMKINTEVRSFGPVSRSGFYLAFODYGCMSLIA 197  
 QY 190 VRYVFRKCPRIIONGAIFOETLSGARSTSLVARGSCINAAEVDVPIILYCNCGGEMV 249  
 DB 198 VRYVFRKCPRIIONGAIFOETLSGARSTSLVARGSCINAAEVDVPIILYCNCGGEMV 257  
 QY 250 PIRGCMCKAGFEAVENGTVGRGCPSTFRANQDEACTHCPIINSRTTSGAINTVCVRNGY 309  
 DB 258 PIRGCMCKAGFEAVENGTVGRGCPSTFRANQDEACTHCPIINSRTTSGAINTVCVRNGY 317  
 QY 310 YRADLPLMPCCTTISAPAVISSVNETSLMEPPDPSGREGVLVNIITCKSGSGR 369  
 DB 318 YRADLPLMPCCTTISAPAVISSVNETSLMEPPDPSGREGVLVNIITCKSGSGR 377  
 QY 370 GACTRCGDNVQVAPROGLTETPRITSLDLAHTQYTFEIIQAVNGVTDQSPFSPASVNI 429  
 DB 378 GACTRCGDNVQVAPROGLTETPRITSLDLAHTQYTFEIIQAVNGVTDQSPFSPASVNI 437

QY 430 TTNQAAPSAVSIMHOVERTVDSITLSWSOPDQPNGLVDLELOYYEKELSEYNATAIKSP 489  
 DB 438 TTNQAAPSAVSIMHOVERTVDSITLSWSOPDQPNGLVDLELOYYEKELSEYNATAIKSP 497  
 QY 490 TNYTVGKLKAGAIYVQVRAIVYAGIRYSGKNYFOTMTBAEYQISIOEKLPIIISGA 549  
 DB 498 TNYTVGKLKAGAIYVQVRAIVYAGIRYSGKNYFOTMTBAEYQISIOEKLPIIISGA 557  
 QY 550 AGVFLAVVIAVAVCRRRGERADSEYTDLOHYSGHNTPGKIIYIDFTYEDPNEAV 609  
 DB 558 AGVFLAVVIAVAVCRRRGERADSEYTDLOHYSGHNTPGKIIYIDFTYEDPNEAV 617  
 QY 610 REPAKEIDISCVKIEOYIAGSEFGEVCSGHIKLPKKEIFVAIKTLKSGYTEKORDPFLS 669  
 DB 618 REPAKEIDISCVKIEOYIAGSEFGEVCSGHIKLPKKEIFVAIKTLKSGYTEKORDPFLS 677  
 QY 670 EASIMGQDENNVHLHGVTYKTSPPVMTIEPEMNSGLDSFTRNDQGFVIOVGMLRG 729  
 DB 678 EASIMGQDENNVHLHGVTYKTSPPVMTIEPEMNSGLDSFTRNDQGFVIOVGMLRG 737  
 QY 730 IAAGKYLADNNYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPYTSALGKIP 789  
 DB 738 IAAGKYLADNNYVHRDLAARNILVNSNLVCKVDFGLSRFLEDDTSDPYTSALGKIP 797  
 QY 790 IRTWAPENIQYRKTSASDVWSYGIWVMEVNSYGERPYMTNODVINALIODYRLPPM 849  
 DB 798 IRTWAPENIQYRKTSASDVWSYGIWVMEVNSYGERPYMTNODVINALIODYRLPPM 857  
 QY 850 DCPBALHQLMDCQXKRNHRPKFGQIVNTLDKXIRPNLSLKMAPLSSGINPLDRTI 909  
 DB 858 DCPBALHQLMDCQXKRNHRPKFGQIVNTLDKXIRPNLSLKMAPLSSGINPLDRTI 917  
 QY 910 PDYTSFNTDWEMLAIKMGQYKESFANAAGTSPVVSQMMEDILRGVTLAHOXKILN 969  
 DB 918 PDYTSFNTDWEMLAIKMGQYKESFANAAGTSPVVSQMMEDILRGVTLAHOXKILN 977  
 QY 970 SIQVRAQMNQIOGVEV 986  
 DB 978 SIQVRAQMNQIOGVEV 994

RESULT 3  
 EPH2 CHICK  
 ID EPH2 CHICK STANDARD; PRT; 1004 AA.  
 AC P28653;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor CEK5).  
 DE EPHB2 OR CEK5.  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
 RC Tissue=Embryo;  
 RX MEDLINE=9214672; PubMed=1664238;  
 RA Pasquale E.B.;  
 RT "Identification of chicken embryo tyrosine kinase 5, a developmentally regulated receptor-type tyrosine kinase of the Eph family.";  
 RL Cell Regul. 2:523-534 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).  
 RC Tissue=Brain;  
 RX MEDLINE=93286394; PubMed=8510926;  
 RA Sajjadi F.G., Pasquale E.B.;  
 RT "Five novel avian Eph-related tyrosine kinases are differentially expressed.";  
 RL Oncogene 8:1807-1813 (1993).

CC - FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. PROBABLY AN  
CC IMPORTANT COMPONENT OF SIGNAL TRANSDUCTION PATHWAYS.  
CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC - SUBCELLULAR LOCATION: Type I membrane protein.  
CC - ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=2:  
CC Name=long; Synonyms=CEK5+;  
CC IsoId=P28693-1; Sequence=displayed;  
CC Name=short;  
CC IsoId=P28693-2; Sequence=VSP\_003018;  
CC - TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION THROUGHOUT  
CC DEVELOPMENT AND SUSTAINED EXPRESSION IN ADULT BRAIN. THE LONGER  
CC FORM (CEK5+) IS SPECIFICALLY EXPRESSED IN THE CENTRAL NERVOUS  
CC SYSTEM.  
CC - SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
CC - SIMILARITY: Contains 2 fibronectin type III domains.  
CC - SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
CC receptor subfamily.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL, M63325; AAA48667.1; ALT\_INIT.  
DR PDB, 1S9G; 06-OCT-99.  
DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR001090; Ephrin\_receptor.  
DR InterPro: IPR008957; FN\_III-like.  
DR InterPro: IPR003961; FN\_III.  
DR InterPro: IPR008978; Gal\_bind\_like.  
DR InterPro: IPR007719; Prot\_kinase.  
DR InterPro: IPR001660; SAM.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR InterPro: IPR008266; Tyr\_kinase\_AS.  
DR InterPro: IPR001426; YKase\_receptor\_V.  
DR Pfam: PF01404; Eph\_Ibd\_1.  
DR Pfam: PF00041; fn3\_2.  
DR Pfam: PF00069; Pkinase\_1.  
DR Pfam: PF00536; SAM\_1.  
DR PRINTS; PR00014; FNTYPEIII.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00615; Eph\_Ibd\_1.  
DR SMART; SM00060; FN3\_2.  
DR SMART; SM00454; SAM; 1.  
DR SMART; SM00219; TYKc; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
KM Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing;  
KM Repeat; 3d-structure; 19  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 1004 EPHRIN TYPE-B RECEPTOR 2.  
FT DOMAIN 20 544 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 545 565 POTENTIAL.  
FT DOMAIN 566 1004 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 20 321 CYS-RICH.  
FT DOMAIN 326 419 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 437 521 FIBRONECTIN TYPE-III 2.  
FT DOMAIN 639 902 PROTEIN KINASE.  
FT DOMAIN 931 995 SAM.

FT SITE 1002 1004 PDZ-BINDING MOTIF (POTENTIAL).  
FT NP\_BIND 645 653 ATP (BY SIMILARITY).  
FT BINDING 671 671 ATP (BY SIMILARITY).  
FT ACT\_SITE 764 764 BY SIMILARITY.  
FT MOD\_RES 614 614 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 620 620 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 798 798 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT MOD\_RES 948 948 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 483 483 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPIC 591 606 Missing (in isoform short).  
FT /FtId=Vsp\_003018  
SQ SEQUENCE 1004 AA; 11963 MW; 8D2621970ECCEB0 CRC64;  
Query Match 95.9%; Score 4975.5; DB 1; Length 1004;  
Best Local Similarity 94.3%; Pred. No. 1.2e-305;  
Matches 937; Conservative 28; Mismatches 12; Indels 17; Gaps 2;  
10 LLLPLAAVEETLMDSTTATAEIGMWHPPSGHEVSGYDENNTARTTYQVNCVFESSQ 69  
11 LALPLAAVEETLMDSTTATAEIGMWHPPSGHEVSGYDENNTARTTYQVNCVFESSQ 70  
70 NNMILRTKFIIRRGARHIVENKFSVDCSSIPSPGSCKETFNLYYEADPDSATKTFPPN 129  
71 NNMILRTKFIIRRGARHIVENKFSVDCSSIPSPGSCKETFNLYYEADPDSATKTFPPN 130  
130 WMENPWVAVDTIAADESPQVDLGRVWKINTEVRSFGPVSRSGFYLAFOYGGCMSLIA 189  
131 WMENPWVAVDTIAADESPQVDLGRVWKINTEVRSFGPVSRSGFYLAFOYGGCMSLIA 190  
190 VVVFYKCPRIIONGALFOETLSGAESTSLVAARGSCJANAEVDVPIKLYCNGGEMTLV 249  
191 VVVFYKCPRIIONGALFOETLSGAESTSLVAARGSCJANAEVDVPIKLYCNGGEMTLV 250  
250 PIGRCMCKAGEAVENGTVGRCGSPGTFKANQSGEACTHCPINSRTTSEGAIVCYCRNGY 309  
251 PIGRCMCKAGEAVENGTVGRCGSPGTFKANQSGEACTHCPINSRTTSEGAIVCYCRNGY 310  
310 YRADLDPLMDPCTTIPSAQAVISSVNETSLMETPRDSCGSEDLVYNIICKSCSGR 369  
311 YRADLDPLMDPCTTIPSAQAVISSVNETSLMETPRDSCGSEDLVYNIICKSCSGR 370  
370 GACTRCGDNVQYARQGLTEPRYISDLIAHTQYFTEIQAVNGVTQSPSPQFASVNI 429  
371 GACTRCGDNVQYARQGLTEPRYISDLIAHTQYFTEIQAVNGVTQSPSPQFASVNI 430  
430 TTNQAPSAVASIMQVSRVTSITLSMSQPDQNGVILDELQYEEKNLSEINTAVVSP 489  
431 TTNQAPSAVASIMQVSRVTSITLSMSQPDQNGVILDELQYEEKNLSEINTAVVSP 490  
490 TTNVVOGLKAGATVFEQVARTVAGYGRYSGKMYFCMTAEVQTSIOECLPIIGSSA 549  
491 TTNVVOGLKAGATVFEQVARTVAGYGRYSGKMYFCMTAEVQTSIOECLPIIGSSA 550  
550 AGVFLAVVIAIVCN-RGFEPADSEYDKLOHTYSGH-----MTFG 592  
551 AGVFLAVVIAIVCN-RGFEPADSEYDKLOHTYSGH-----MTFG 593  
593 MKIYIDPFTYEDPNEAVSEFAKEIDISCVKLEQVIGAGEFEVSGSHKLPGRKEIFVAI 652  
611 MKIYIDPFTYEDPNEAVSEFAKEIDISCVKLEQVIGAGEFEVSGSHKLPGRKEIFVAI 670  
653 KTKSGYTEKORPDLSEASIMQGFDEHNVILHGVYTKSTPVMITTEFMNGSLDSFLR 712  
671 KTKSGYTEKORPDLSEASIMQGFDEHNVILHGVYTKSTPVMITTEFMNGSLDSFLR 730  
713 QNDGQFTYICVGMIRGIAAGMKYLADNMYVHRPLAARNILVSNILVCYKSDPGLSRFLE 772  
731 QNDGQFTYICVGMIRGIAAGMKYLADNMYVHRPLAARNILVSNILVCYKSDPGLSRFLE 790

QY 773 DDTSDPTVYTSALGKIPIRKFTAPALQYRKFTASDVWSYGIYMEVMSYGERPYDMMN 832  
 Db 791 DDTSDPTVYTSALGKIPIRKFTAPALQYRKFTASDVWSYGIYMEVMSYGERPYDMMN 850  
 QY 833 QDVNMAFEQDYRLPEPMDCPSALHQLMLDCQKDRNRHPRFGQIVNTLDMKINPMSLXA 892  
 Db 851 QDVNMAFEQDYRLPEPMDCPSALHQLMLDCQKDRNRHPRFGQIVNTLDMKINPMSLXA 910  
 QY 893 MAPLSSGGINPLDRTIPDYTSFNTVDEMLAIRMGOYKESFPAAGTSDVTSQMMED 952  
 Db 911 MAPLSSGGINPLDRTIPDYTSFNTVDEMLAIRMGOYKESFPAAGTSDVTSQMMED 970  
 QY 953 ILRLGVTLAHHOKKILNSIQVMAQNNQIOSVEV 986  
 Db 971 ILRLGVTLAHHOKKILNSIQVMAQNNQIOSVEV 1004

RESULT 4  
 EPH2\_COTVA STANDARD; PRT; 987 AA.  
 ID EPH2\_COTVA STANDARD; PRT; 987 AA.  
 AC 090344;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor QEEKS).  
 GN EPH2 OR QEEKS.  
 OS Coturnix coturnix japonica (Japanese quail).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.  
 OC NCBI\_TaxID=93934;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=96109331; PubMed=8612986;  
 RA Kenny D., Bromner-Frazer M., Marcelle C.;  
 RT "The receptor tyrosine kinase QEEKS mRNA is expressed in a gradient within the neural retina and the tectum.";  
 RL Dev. Biol. 172:708-716(1995).  
 CC -1- FUNCTION: Receptor for members of the ephrin-B family.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.  
 CC -----  
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 CC -----  
 DR EMBL; X91737; CAAG2862.1; -;  
 DR HSSP; P29323; 1B4F.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003963; FNIII\_subd.  
 DR InterPro; IPR008978; Gal\_bind\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008265; Tyr\_kinase\_AS.  
 DR InterPro; IPR001426; YKase\_receptorV.  
 DR Pfam; PF01404; EPH\_1bd. 1.  
 DR Pfam; PF00041; fn3\_2.  
 DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PS00014; FNYPE11.  
 DR PRINTS; PS00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00645; EPH\_1bd. 1.  
 DR SMART; SM00060; FN3\_2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TYKC; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; FALSE\_NEG.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS50105; SAM\_DOMAIN; 1.  
 DR TRANSFERASE; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 KW SIGNAL  
 FT SIGNAL 1  
 FT CHAIN 20 987  
 FT DOMAIN 20 544  
 FT TRANSMEM 545 565  
 FT DOMAIN 566 987  
 FT DOMAIN 185 322  
 FT DOMAIN 323 432  
 FT DOMAIN 433 530  
 FT DOMAIN 622 885  
 FT DOMAIN 914 978  
 FT SINE 985 987  
 FT NP\_BIND 628 636  
 FT BINDING 654 654  
 FT ACT\_SITE 747 747  
 FT MOD\_RES 597 597  
 FT MOD\_RES 603 603  
 FT MOD\_RES 781 781  
 FT MOD\_RES 931 931  
 FT CARBOHYD 266 266  
 FT CARBOHYD 337 337  
 FT CARBOHYD 429 429  
 FT CARBOHYD 478 478  
 FT CARBOHYD 483 483  
 SQ SEQUENCE 987 AA; 110331 MW; 05D6C68B718D07 CRC64;  
 Query Match 95.3%; Score 4945; DB 1; Length 987;  
 Best Local Similarity 94.9%; Pred. No. 9.5e-304;  
 Matches 927; Conservative 30; Mismatches 20; Indels 0; Gaps 0;  
 QY 10 LLLPLAAVEETLMDSTTATAEELGMVHPSPGWEVEVSGYDENNTIRYQVCNVESSQ 69  
 Db 11 LALLPLAAVEETLMDSTTATAEELGMVHPSPGWEVEVSGYDENNTIRYQVCNVESSQ 70  
 QY 70 NNMILTKFIRRGARHIVHEKESVRCSSIPVPSCKETFNLYYEADPDSATKTFN 129  
 Db 71 NNMILTKFIRRGARHIVHEKESVRCSSIPVPSCKETFNLYYEADPDSATKTFN 130  
 QY 130 WNEPVMVVDITIADESFSQVDLGRVMKINTVRSFGPVSRSGFYLAPODYGCMSLIA 189  
 Db 131 WNEPVMVVDITIADESFSQVDLGRVMKINTVRSFGPVSRSGFYLAPODYGCMSLIA 190  
 QY 190 VRFVPRKCPRIIINGAIFQETLSAESTSLVAARCSIIANAEBVDVPIKYCNGDEGLV 249  
 Db 191 VRFVPRKCPRIIINGAIFQETLSAESTSLVAARCSIIANAEBVDVPIKYCNGDEGLV 250  
 QY 250 PIGRCMKAGFEAVENGTVCGSPGSGTFKANOGEACTHCPINSRTSSEGAATVCNGY 309  
 Db 251 PIGRCMKAGFEAVENGTVCGSPGSGTFKANOGEACTHCPINSRTSSEGAATVCNGY 310  
 QY 310 YRADLDPLDMECTTIPAPQAVISSVNETSLMTEWTPPRDSGGREDIVNIICKSCSGSR 369  
 Db 311 YRADLDPLDMECTTIPAPQAVISSVNETSLMTEWTPPRDSGGREDIVNIICKSCSGSR 370  
 QY 370 GACTRCGNVOYARQIGTEPRRIYISDLAHTQYTEILQAVNGVMDQSPFSPQASVNI 429



```

Db 371 GACTRCGDNVQFAPRQJGLTEPRRIYISDLLAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 430
QY 430 TTNOAPSAVSIMHOVSRTVDSITLWSOPDPNGVILDELOVEKELESEYNATAIKSP 489
Db 431 TTNOAPSAVSIMHOVSRTVDSITLWSOPDPNGVILDELOVEKELESEYNATAIKSP 490
QY 490 TMTVVOGLKAGAIYFVOYFARTVAGYGRYSGMYFQMTAEFYOTSIOEKPLIIGSSA 549
Db 491 TMTVVOGLKAGAIYFVOYFARTVAGYGRYSGMYFQMTAEFYOTSIOEKPLIIGSSA 550
QY 550 AGIVFLIAVVVIAIVCNRRGFPERADSEYTDKLOHTSGHMTPGMKIYIDPFTYEDPNEAV 609
Db 551 AGIVFLIAVVVIAIVCNRRGFPERADSEYTDKLOHTSGHMTPGMKIYIDPFTYEDPNEAV 610
QY 610 REFAKEIDISCVKIEQYIGAGEFGEVCSGHLKLPKKEIFVAIKTLKSGYTEKORRDFLS 669
Db 611 REFAKEIDISCVKIEQYIGAGEFGEVCSGHLKLPKKEIFVAIKTLKSGYTEKORRDFLS 670
QY 670 BASIMGQFDPHNVYHLEGVTKSTPVWITTEFMENGLSDSFLRQNDGQFTVIQVGMIRG 729
Db 671 BASIMGQFDPHNVYHLEGVTKSTPVWITTEFMENGLSDSFLRQNDGQFTVIQVGMIRG 730
QY 730 IAAGMXYLADNMYVHRDLARNTLVNSNLVCKVSDGLSRFLEDDTSDPTYSALGKIP 789
Db 731 IAAGMXYLADNMYVHRDLARNTLVNSNLVCKVSDGLSRFLEDDTSDPTYSALGKIP 790
QY 790 IRMTAPEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAIEQDYRLPPM 849
Db 791 IRMTAPEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAIEQDYRLPPM 850
QY 850 DCPSAIHQMLDCWQKDRNHRPKFGQIVNTLDMIRNPNSLKAMAPLSSGINPLDRTI 909
Db 851 DCPSAIHQMLDCWQKDRNHRPKFGQIVNTLDMIRNPNSLKAMAPLSSGINPLDRTI 910
QY 910 PDYTSFNTVDEMLEAIKMGQYKESFANAGFTSFDVVSOMMEDILRLGYTLAGHCKKILN 969
Db 911 PDYTSFNTVDEMLEAIKMGQYKESFANAGFTSFDVVSOMMEDILRLGYTLAGHCKKILN 970
QY 970 SIQVMAQNNQIQSVY 986
Db 971 SIQVMAQNNQIQSVY 987

```

Search completed: August 28, 2004, 04:09:26  
 Job time : 20.3577 secs

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Gencore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:02:25 ; Search time 31.8844 seconds  
(without alignments)  
2974.650 Million cell updates/sec

Title: US-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MALRLGALLLPLLAIVE.....INSLGVRAQNMQIQSVEV 986

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5089	98.1	970	2	receptor protein-t
2	4993.5	96.3	995	2	embryo kinase 5 -

ALIGNMENTS

RESULT 1  
178842  
receptor protein-tyrosine kinase - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #ext\_change 16-Jun-1999  
C:Accession: I78842  
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welch,  
Oncogene 10, 897-905, 1995  
A:Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty  
A:Reference number: 158351; MUID:95206782; PMID:7898931  
A:Accession: I78842  
A:Status: preliminary; translated from GB/EMBL/DDBI  
A:Molecule type: mRNA  
A:Residues: 1-970 <RES>  
A:Cross-references: GB:U36643; NID:9551609; PIDN:AAA74244.1; PID:9551610  
C:Genetics:  
A:Gene: HEK5  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
F:603-871/Domain: protein kinase homology <KIN>  
F:894-960/Domain: SAM homology <SAM>

Query Match 98.1% ; Score 5089 ; DB 2 ; Length 970 ;

Best Local Similarity 99.4% ; Pred. No. 5.3e-231 ;  
Matches 966 ; Conservative 2 ; Mismatches 2 ; Indels 2 ; Gaps 1 ;

QY	15	LLAAVEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYQVGNVFESSQNMRL 74
DB	1	LLAAVEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYQVGNVFESSQNMRL 60
QY	75	TKPIRRGARRHYEMKSVSDCSSIPSPGCKETFLNLYYEADPFPSATCFPMWENP 134
DB	61	TKPIRRGARRHYEMKSVSDCSSIPSPGCKETFLNLYYEADPFPSATCFPMWENP 120
QY	135	WVKVDTIADESFSQVDIGRVMKINTEVRSFGVSRSGFYLAQDYGGCNSLAVRYFY 194
DB	121	WVKVDTIADESFSQVDIGRVMKINTEVRSFGVSRSGFYLAQDYGGCNSLAVRYFY 180
QY	195	RKCPRIIONGALFOETLSGASTSLVARGSCINAEEDVPILKYCNGDEMLVPIGRG 254
DB	181	RKCPRIIONGALFOETLSGASTSLVARGSCINAEEDVPILKYCNGDEMLVPIGRG 240
QY	255	MCKAGFEAVENGTVRCGCPGCTFKANQGDCACTHCPIINSRTTSGATNCVCRNGYRADL 314
DB	241	MCKAGFEAVENGTVRCGCPGCTFKANQGDCACTHCPIINSRTTSGATNCVCRNGYRADL 300
QY	315	DPLDMPCTTISAPQAVTSSVNETSLMLEWTPPRDSGREDLVNITCKSGSGRGACTR 374
DB	301	DPLDMPCTTISAPQAVTSSVNETSLMLEWTPPRDSGREDLVNITCKSGSGRGACTR 360
QY	375	CGDNQVAPROGLTEPRITYSDLAHTQYTFEIOAVNGVTDQSPSPQFASVNTTNOA 434
DB	361	CGDNQVAPROGLTEPRITYSDLAHTQYTFEIOAVNGVTDQSPSPQFASVNTTNOA 420
QY	435	APSAVSIMHOVSRTVDSITLMSQPDQNGVILDEYLOVYKEISEYNALAKSPNTVT 494
DB	421	APSAVSIMHOVSRTVDSITLMSQPDQNGVILDEYLOVYKEISEYNALAKSPNTVT 480
QY	495	VQGLKAGAIYFQVQARIVAGYGRSGKMFQMTAEAYQISIEKPLITIGSSAAGLVF 554
DB	481	-GLKAGAIYFQVQARIVAGYGRSGKMFQMTAEAYQISIEKPLITIGSSAAGLVF 538
QY	555	LIAVVVIAIVCNRRGFERADSEYTDKLOHTYSGHMTPMKTIYIDPFYEDPNEAVREFAK 614
DB	539	LIAVVVIAIVCNRRGFERADSEYTDKLOHTYSGHMTPMKTIYIDPFYEDPNEAVREFAK 598
QY	615	EIDISCYKLEOVYTAGFEGVCSGHLKPKGREIFVAIKTILKSGYTERQQRDPLSEASIM 674
DB	599	EIDISCYKLEOVYTAGFEGVCSGHLKPKGREIFVAIKTILKSGYTERQQRDPLSEASIM 658
QY	675	GOFDHPNTYHLEGVYTKSTPVMIIITEFMENGLSDSFLEQNDGQFTVIOVQMLGIAAGM 734
DB	659	GOFDHPNTYHLEGVYTKSTPVMIIITEFMENGLSDSFLEQNDGQFTVIOVQMLGIAAGM 718
QY	735	KYLADMTYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSDPTYSALGCKPIRRTA 794
DB	719	KYLADMTYVHRDLAARNILVNSNLVCKVSDFGLSRFLLEDOTSDPTYSALGCKPIRRTA 778
QY	795	PBAIOYRKFTASDVMSYGIYVWEVMSYGERPYMDMTQDYINALEQYRPLPPEDCSA 854
DB	779	PBAIOYRKFTASDVMSYGIYVWEVMSYGERPYMDMTQDYINALEQYRPLPPEDCSA 838
QY	855	LHQLMDCQKDRNRPRFGQIVNTLDKIRNPNLSLKMAPLSSGINSPLDRTIPDYTS 914
DB	839	LHQLMDCQKDRNRPRFGQIVNTLDKIRNPNLSLKMAPLSSGINSPLDRTIPDYTS 898
QY	915	FNTVDEWLEATIMQGYKESFANAGTSPDYVSOMMMEDILLAGVLAHOKKILNSIQVM 974
DB	899	FNTVDEWLEATIMQGYKESFANAGTSPDYVSOMMMEDILLAGVLAHOKKILNSIQVM 958
QY	975	RAQNMQIQSVEV 986
DB	959	RAQNMQIQSVEV 970

RESULT 2

A56599 embryo kinase 5 - chicken  
N/Alternate names: receptor tyrosine kinase Ceks  
N/Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C/Species: Gallus gallus (chicken)  
C/Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 04-Feb-2000  
C/Accession: A56599  
R/Pasquale, E.B.  
Cell Regul. 2, 523-534, 1991  
A/Title: Identification of chicken embryo kinase 5, a developmentally regulated receptor  
A/Reference number: A56599; MUID:92144672; PMID:1664238  
A/Accession: A56599  
A/Status: Preliminary  
A/Molecule type: mRNA  
A/Residues: 1-995 <PMS>  
A/Cross-References: GB:M62325; NID:g211448; PIDN:AAA48667.1; PID:g211449  
A/Note: Sequence extracted from NCBI backbone (NCBI:81999; NCBI:P:82001)  
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat  
C/Keywords: Atp; phosphotransferase; transmembrane protein; tyrosine-specific protein ki  
F:628-896/Domain: protein kinase homology <KIN>  
F:636-644/Region: protein kinase ATP-binding motif  
F:919-985/Domain: SAM homology <SAM>

Query Match 96.3%; Score 4993.5; DB 2; Length 995;  
Best Local Similarity 95.8%; Pred. No. 1.6e-226;  
Matches 937; Conservative 28; Mismatches 12; Indels 1; Gaps 1;

QY 10 LLLPLAAVETIMDSTTAELGMYHPHPSGMEVSYGDEMMNTIRTYQVQNVFSSQ 69  
DB 18 LALLPLAAVEETIMDSTTAELGMYHPHPSGMEVSYGDEMMNTIRTYQVQNVFSSQ 77  
QY 70 NNMLRTYFIRRRGAHRIHVEKFSVRDSSIPSVPGSCKETFNLYYEADFDSATKTFPN 129  
DB 78 NNMLRTYFIRRRGAHRIHVEKFSVRDSSIPSVPGSCKETFNLYYEADFDSATKTFPN 137  
QY 130 WMENPMKVDITADBSFSQVDLGRVYKINTEVRSFGVSRSGFIYAFQDYGCMSLIA 189  
DB 138 WMENPMKVDITADBSFSQVDLGRVYKINTEVRSFGVSRSGFIYAFQDYGCMSLIA 197  
QY 190 VRVYRKCPRRIIONGAIFOETISGAEISTLVAARGSCIANAEVDPVIRKLCNGDEWLY 249  
DB 198 VRVYRKCPRRIIONGAIFOETISGAEISTLVAARGSCIANAEVDPVIRKLCNGDEWLY 257  
QY 250 PIGRCMKAGFEAVENGTCVRCGSPGTFKANKQDEACTHCPINSRTTBGATNCVCRNGY 309  
DB 258 PIGRCMKAGFEAVENGTCVRCGSPGTFKANKQDEACTHCPINSRTTBGATNCVCRNGY 317  
QY 310 YRADDLPDMPCTTIPAPQAVISSVNETSLMLETPRDSGGREDLVYNIICKSGSGSR 369  
DB 318 YRADDLPDMPCTTIPAPQAVISSVNETSLMLETPRDSGGREDLVYNIICKSGSGSR 377  
QY 370 GACTRCGDNVQYAPRQGLTEPRYISDLAHTQYTFEIQAVNGVTDQSPFPQFASVNI 429  
DB 378 GACTRCGDNVQYAPRQGLTEPRYISDLAHTQYTFEIQAVNGVTDQSPFPQFASVNI 437  
QY 430 TTNOAPSAYSIMQVSRVDSITLSWQDQPNQVTLDELQYERKELSEVNAATIKSP 489  
DB 438 TTNOAPSAYSIMQVSRVDSITLSWQDQPNQVTLDELQYERKELSEVNAATIKSP 497  
QY 490 TINTVVOGLKAGAIYVQVBARTVAGYGRYSGMYFQMTAEYQTSIOEKLPLIIGSSA 549  
DB 498 TINTVVOGLKAGAIYVQVBARTVAGYGRYSGMYFQMTAEYQTSIOEKLPLIIGSSA 557  
QY 550 AGLYFLAAVYVIAVCN-REGFERADESYTDKLOHTSGHMPGMKIYIDPFYEDPNEA 608  
DB 558 AGLYFLAAVYVIAVCN-REGFERADESYTDKLOHTSGHMPGMKIYIDPFYEDPNEA 617  
QY 609 VREFAKEIDISCVKIEOVIGAGEFEGVSGHLKLPGRKEIFVAIKTLKSGYTEKQRRFL 668  
DB 618 VREFAKEIDISCVKIEOVIGAGEFEGVSGHLKLPGRKEIFVAIKTLKSGYTEKQRRFL 677  
QY 669 SEASIMQGFHPNVITHLEGVYTKSTPVMITTEMNGSLDSFLQNDGQFTVQLVGMNR 728

DB 678 SEASIMQGFHPNVITHLEGVYTKSTPVMITTEMNGSLDSFLQNDGQFTVQLVGMNR 737  
QY 729 GIAGMKYIADNNVYHRDLAARNILVNSNLYCVKXSDFGLSRFLBDDTSDFPTYSALGGKI 788  
DB 728 GIAGMKYIADNNVYHRDLAARNILVNSNLYCVKXSDFGLSRFLBDDTSDFPTYSALGGKI 797  
QY 789 PIRMTAPPAIDYRKFTSASDVMSYGIYVWEVMSYGERPYMTQDVYNAIEODYRLLPP 848  
DB 788 PIRMTAPPAIDYRKFTSASDVMSYGIYVWEVMSYGERPYMTQDVYNAIEODYRLLPP 857  
QY 849 MDCEPALHQLMDQWQXDRNHRPKFGQIVNTLDKXIRNPNSLKAMAPLSSGINTPLDRT 908  
DB 858 MDCEPALHQLMDQWQXDRNHRPKFGQIVNTLDKXIRNPNSLKAMAPLSSGINTPLDRT 917  
QY 909 IPDYTSRTYDENVLEATMGQYKESFANAGFTSFQVYQMMEDILRLGVTLAGHOKKIL 968  
DB 918 IPDYTSRTYDENVLEATMGQYKESFANAGFTSFQVYQMMEDILRLGVTLAGHOKKIL 977  
QY 969 NSIQYMRQNMQIQSVEY 986  
DB 978 NSIQYMRQNMQIQSVEY 995

Search completed: August 28, 2004, 04:14:04  
Job time: 31.8844 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 28, 2004, 04:00:54 ; Search time 97.1024 Seconds

(without alignments)  
3203.844 Million cell updates/sec

Title: US-09-914-883-2

Perfect score: 5188

Sequence: 1 MALRLGALLLPLLAWE.....LINSIQVFAQMNQIQSVEV 986

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 90%

Maximum Match 100%

Listing first 45 summaries

## Database :

1: SP\_archaea:\*  
2: SP\_bacteria:\*  
3: SP\_fungi:\*  
4: SP\_human:\*  
5: SP\_invertebrate:\*  
6: SP\_mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP Vertebrate:\*  
14: SP\_unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5130	98.9	994	11	Q9GVY4 Q9GVY4 mus sp. neu

## ALIGNMENTS

RESULT 1  
Q9GVY4 PRELIMINARY; PRT; 994 AA.  
AC Q9GVY4; 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Neutral kinase, NUK=EPH/ELK/ECK family receptor-like tyrosine kinase (EC 2.7.1.112) (Ephrin receptor) (Tyrosine-protein kinase receptor).

OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10095;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94181250; PubMed=8134103;  
RA Henkemeyer N., Marengue L.E., Mogliade J., Olivier J.P., Conlon R.A.,  
RA Holtmeyer D.P., Letvan K., Pawson T.,  
RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles  
RT in segmental patterning of the brain and axonogenesis.",  
RL Oncogene 9:1001-1014(1994).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
CC TYROSINE PHOSPHATE  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. EPHRIN  
CC RECEPTOR SUBFAMILY.  
CC HSSP; P29323; 184F.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0005003; F:ephrin receptor activity; IEA.  
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.  
DR InterPro; IPR006309; EGF-like.  
DR InterPro; IPR001890; Ephrin\_receptor.  
DR InterPro; IPR003962; Fh11\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008857; FN\_III-like.  
DR InterPro; IPR008879; Gal\_bind\_like.  
DR InterPro; IPR000719; Prol\_kinase.  
DR InterPro; IPR001660; SAM.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR InterPro; IPR001426; Ykase\_receptorov.  
DR Pfam; PF01404; EPH\_1bd; 1.  
DR Pfam; PF00041; fn3; 2.  
DR Pfam; PF00069; kinase; 1.  
DR Pfam; PF00536; SAM; 1.  
DR PRINTS; PR00014; ENTPEPIL.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00615; EPH\_1bd; 1.  
DR SMART; SM00060; FN3\_2.  
DR SMART; SM00454; SAM; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
DR PROSITE; PS50105; SAM\_DOMAIN; 1.  
DR AP; binding; Glycoprotein; Kinase; Phosphorylation; Receptor; Repeat;  
KW Transferrase; Transmembrane; Tyrosine-protein kinase.  
SQ SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64;

Query Match 98.9%; Score 5130; DB 11; Length 994;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 10 LLLPLLAVEETLMDSTTATAELGMYVPPSGMEVSGYDENMNTIRTYQVGVFESSQ 69  
DB 18 LLLPLLAVEETLMDSTTATAELGMYVPPSGMEVSGYDENMNTIRTYQVGVFESSQ 77  
QY 70 NNMWLATKIRRGARIRIVEMKFSVPCSSIPSPGSKETFFNLYYVADSDATKTFPN 129  
DB 78 NNMWLATKIRRGARIRIVEMKFSVPCSSIPSPGSKETFFNLYYVADSDATKTFPN 137  
QY 130 WNEPVMVYVDLIADESFQVDLGGVVKKINTEVRSFGPVSRSGFYLAFDYGGCMSLIA 189

Db 138 WMEPWYXVDITIADEFSQVLDLGRYMKINTEVRSFGVSRNGFYIAFODYGGCKSLIA 197  
QY 190 VRVYFKCPRIIONGAIFOETLSGABSTSLVAARGSCIANAEVDPYIKLYCNGDEWLV 249  
Db 198 VRVYFKCPRIIONGAIFOETLSGABSTSLVAARGSCIANAEVDPYIKLYCNGDEWLV 257  
QY 250 PIGCMCKAGFEAVENGTVCRCGSPGTFKANOGBEACTHCPIINSRTTSEGATNCVCRRNGY 309  
Db 258 PIGCMCKAGFEAVENGTVCRCGSPGTFKANOGBEACTHCPIINSRTTSEGATNCVCRRNGY 317  
QY 310 YRADLDPLDMPCTTIPAPQAVISSVNETSLMLEWTPPRDSCGREDLVYNIICKSCGSGR 369  
Db 318 YRADLDPLDMPCTTIPAPQAVISSVNETSLMLEWTPPRDSCGREDLVYNIICKSCGSGR 377  
QY 370 GACTRCGDNYOYAPROGLTEPRITYSDLAHTOYTFEIOAVNGVTDQSPESPQFASVNI 429  
Db 378 GACTRCGDNYOYAPROGLTEPRITYSDLAHTOYTFEIOAVNGVTDQSPESPQFASVNI 437  
QY 430 TTNOAPSASVSIHMOVSRTVDSITLSWSQDPQNGVILDYELOYEKELSEYNATAIKSP 489  
Db 438 TTNOAPSASVSIHMOVSRTVDSITLSWSQDPQNGVILDYELOYEKELSEYNATAIKSP 497  
QY 490 TMTVTVOGLKAGAIYVQVQARTVAGYGRYSKMYFQMTFAEYQTSIOEKLPIIIGSSA 549  
Db 498 TMTVTVOGLKAGAIYVQVQARTVAGYGRYSKMYFQMTFAEYQTSIOEKLPIIIGSSA 557  
QY 550 AGLEVFLAVVYIAIVCNRSGFERADSEYTDKLOHYTSGHMPGMKIYIDPFTYEDPNEAV 609  
Db 558 AGLEVFLAVVYIAIVCNRSGFERADSEYTDKLOHYTSGHMPGMKIYIDPFTYEDPNEAV 617  
QY 610 REFAKEIDICVYIEQYIGAGEFGEVCSGHLKLPKREIFVAIKTILKSGYTEKORDPLS 669  
Db 618 REFAKEIDICVYIEQYIGAGEFGEVCSGHLKLPKREIFVAIKTILKSGYTEKORDPLS 677  
QY 670 EASIMGQFDHPNYIHLGCVTKSTPYMIITEFMENGLSDSFLRQNDGQFTVIOVGMLRG 729  
Db 678 EASIMGQFDHPNYIHLGCVTKSTPYMIITEFMENGLSDSFLRQNDGQFTVIOVGMLRG 737  
QY 730 IAAQMKYLDMMYVHRDLAARNILVNSNLVCVSDFLSRPLEDDTSDPTYSALGKTP 789  
Db 738 IAAQMKYLDMMYVHRDLAARNILVNSNLVCVSDFLSRPLEDDTSDPTYSALGKTP 797  
QY 790 IRWTAPBAIOYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVYINAIEODYRLPPM 849  
Db 798 IRWTAPBAIOYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVYINAIEODYRLPPM 857  
QY 850 DCPSSALHQLMLDCWQKDRNHRPKFQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTI 909  
Db 858 DCPSSALHQLMLDCWQKDRNHRPKFQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTI 917  
QY 910 PDYTSFNTVDEWELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTLAGHOKKILN 969  
Db 918 PDYTSFNTVDEWELEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTLAGHOKKILN 977  
QY 970 SIQVRAQNMNOIQSEV 986  
Db 978 SIQVRAQNMNOIQSEV 994

Search completed: August 28, 2004, 04:12:52  
Job time : 98.1024 secs

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OM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:04 ; Search time 97.5855 Seconds  
(without alignments)  
2854.849 Million cell updates/sec

Title: US-09-914-883-2  
Perfect score: 5188  
Sequence: 1 MALRRLGAILLLPLLAIVE.....INSTQWRAGMNOISVEV 986

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: geneseqp290ar04:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2002s:\*  
7: geneseqp2003as:\*  
8: geneseqp2003bs:\*  
9: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	5181	99.9	1055	3	AAB19591 Human CAS
2	5181	99.9	1055	6	ABU07847 Human eph
3	5177.5	99.8	987	3	AAB19590 Human CAS
4	5130	98.9	994	2	AAM26366 Mouse Nuk
5	5130	98.9	994	4	AAU01907 Murine ne
6	5126	98.8	994	2	AAAR7018 Receptor
7	5093	98.2	970	2	AAAR5089 Eph-like
8	4993.5	96.3	995	2	AAAR5712 Eph-1-like
9	4971.5	95.8	1011	2	AAAR5709 Eph-relat

ALIGNMENTS

RESULT 1  
AAB19591  
ID AAB19591 standard; protein; 1055 AA.  
XX  
AC AAB19591;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Human CASB616.  
XX  
KW CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2v;

KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
KW ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.  
XX Homo sapiens.  
OS  
XX MO200053216-A2.  
XX  
XX 14-SEP-2000.  
XX  
XX 28-FEB-2000; 2000WO-EP001587.  
XX  
XX 05-MAR-1999; 99GB-00005124.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
XX Vinals Y De Bassolec;  
XX  
XX WPI; 2000-587384/55.  
XX  
XX N-PSDB; AAA88549.  
XX  
XX Vaccine composition for treating ovarian and colon cancer, comprises  
PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
PT expressing the polypeptides.  
XX  
XX Claim 1; Page 42; 57pp; English.  
XX  
XX The present sequence is that of human CASB616, a member of the Eph and  
CC Eph-related family of receptor protein tyrosine kinases. CASB616 is also  
CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616  
CC polypeptides and polynucleotides are important immunogens for specific  
CC prophylactic or therapeutic immunization against tumours, especially  
CC colon cancer (claimed) and ovarian cancer. They are specifically  
CC expressed or highly over-expressed in tumours compared to normal cells  
CC and can thus be targeted by antigen-specific immune mechanisms leading to  
CC destruction of the tumour cells. They can also be used to diagnose the  
CC occurrence of tumour cells. Their inappropriate expression can also cause  
CC an induction of autoimmune responses, which can be corrected through  
CC vaccination using the CASB616 polypeptides or polynucleotides  
XX  
SQ Sequence 1055 AA:  
  
Query Match 99.9%; Score 5181; DB 3; Length 1055;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MALRRLGAILLLPLLAIVEETLMDSTTAETALGWMVHPBSGWEVSGYDENMTIRTYQ 60  
DB 1 MALRRLGAILLLPLLAIVEETLMDSTTAETALGWMVHPBSGWEVSGYDENMTIRTYQ 60  
QY 61 VCNVFESSQNWLTKTFRRGARRIHVEMKFSVSDCSISPSVSGCKETNLVYEADF 120  
DB 61 VCNVFESSQNWLTKTFRRGARRIHVEMKFSVSDCSISPSVSGCKETNLVYEADF 120  
QY 121 DSATTFPNNMENPMVKYDITIADESFSQVDLGRVWKINTEVRSFGVRSRGFYLAFO 180  
DB 121 DSATTFPNNMENPMVKYDITIADESFSQVDLGRVWKINTEVRSFGVRSRGFYLAFO 180  
QY 181 YGGCNSLIARVFRKCRRIITONGAIFQETLSGAFSISLVAAARSCIANAEVDPITLY 240  
DB 181 YGGCNSLIARVFRKCRRIITONGAIFQETLSGAFSISLVAAARSCIANAEVDPITLY 240  
QY 241 CNGDEMIIVPIGRCKKAFVAVENGATVCRGCPGTFKANGDCACTHCPIINSRTSBA 300  
DB 241 CNGDEMIIVPIGRCKKAFVAVENGATVCRGCPGTFKANGDCACTHCPIINSRTSBA 300  
QY 301 TNCVCRNGYRADLPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPPDSGREDLVNI 360  
DB 301 TNCVCRNGYRADLPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPPDSGREDLVNI 360  
QY 361 ICKSGSGRGACTCGDNVQYAPROLGTEPRITYISDLATQYTFEIOANGVTDOSPF 420  
DB 361 ICKSGSGRGACTCGDNVQYAPROLGTEPRITYISDLATQYTFEIOANGVTDOSPF 420

```

QY 421 SPQFASVNTTNOAPSAVSIMHOVSRFTVDSITLSMSQDPQNGVILDELYEKEISE 480
DB 421 SPQFASVNTTNOAPSAVSIMHOVSRFTVDSITLSMSQDPQNGVILDELYEKEISE 480
QY 481 YNAFAISPTNTVVOGLKAGAIYVPOVARTAVAGYGRYSGKXYPOTMTEAEYQTSIOEK 540
DB 481 YNAFAISPTNTVVOGLKAGAIYVPOVARTAVAGYGRYSGKXYPOTMTEAEYQTSIOEK 540
QY 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600
DB 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600
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DB 601 TYEDPNAVAEPAKEIDISCVKIEQYVIGAGEFGEVSGHIXLPKKEITVAITKTKSGYT 660
QY 661 EKORDELSEASIMGOFDHPNVTHLBQVTKSTPVIITEFMENGSLDSFLRQNDGQFTV 720
DB 661 EKORDELSEASIMGOFDHPNVTHLBQVTKSTPVIITEFMENGSLDSFLRQNDGQFTV 720
QY 721 IOVGMIRGIAAGMKYIADNMYHRRDLAARNILVNSNLVCKYSDPGLSFLLEDTSDDPY 780
DB 721 IOVGMIRGIAAGMKYIADNMYHRRDLAARNILVNSNLVCKYSDPGLSFLLEDTSDDPY 780
QY 781 TSAAGKIPRTWAPPAIYQKFTSASDVSYGIWMMWVSGERYMTNODVINAIE 840
DB 781 TSAAGKIPRTWAPPAIYQKFTSASDVSYGIWMMWVSGERYMTNODVINAIE 840
QY 841 QDVRLLPPNDGSAHQMLMDQKDRNHRPKGQIVNLIDKXIRNPNSLKAMAPLISGI 900
DB 841 QDVRLLPPNDGSAHQMLMDQKDRNHRPKGQIVNLIDKXIRNPNSLKAMAPLISGI 900
QY 901 NLPLDRTIPDYTSFNTVDEMLEAIKMGQYKESFAVAGTSPDVYSQMMEDILRLGVTL 960
DB 901 NLPLDRTIPDYTSFNTVDEMLEAIKMGQYKESFAVAGTSPDVYSQMMEDILRLGVTL 960
QY 961 AGHOKILNSIQVMAQMNQIOSVE 985
DB 961 AGHOKILNSIQVMAQMNQIOSVE 985

```

## RESULT 2

ABU07847

ID ABU07847 standard; protein; 1055 AA.

XX AC ABU07847;

DT 10-MAY-2003 (first entry)

DE Human ephrin receptor ligand EphB2.

XX Cytostatic; vasodilator; antiinflammatory; cardiact; gene therapy;  
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;  
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;  
 KW cell migration disorder; cell proliferation disorder; neovascularisation;  
 KW ischemia; infarction; tissue graft; transplant; human;  
 KW ephrin receptor ligand; tie receptor tyrosine kinase; EphB2.

XX OS Homo sapiens.

XX PN WO2003004529-A2.

XX PD 16-JAN-2003.

XX PF 02-JUL-2002; 2002WO-IB005224.

XX PR 02-JUL-2001; 2001US-0302960P.

XX PA (LIGN) LICENTIA LTD.

XX PI Alicate K, Kubo H;

XX WPI; 2003-210341/20.

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DR N-PSDB; ABX12548.
XX Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
XX
PS Disclosure; Page 128-132; 1999p; English.
XX
CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularization (e.g. ischemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human EphB2, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Ephrin receptor ligands
XX
SQ Sequence 1055 AA:

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Query Match 99.9%; Score 5181; DB 6; Length 1055;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 984; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MALRRLGAPALLPLLAAREETLMDSTTATAEIGMWHPSPGWEVSGYDENNTIRTYQ 60
DB 1 MALRRLGAPALLPLLAAREETLMDSTTATAEIGMWHPSPGWEVSGYDENNTIRTYQ 60
QY 61 VCNVFESSQNNWLTKEFIRRRGAHRIHVENKFSVRDCCSIPSPGSCKETENLYYEADP 120
DB 61 VCNVFESSQNNWLTKEFIRRRGAHRIHVENKFSVRDCCSIPSPGSCKETENLYYEADP 120
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DB 121 DSATKTFPNNMENPWWKVDITIADESFSQVLDGRVVKINTEVRSFGPSRSGFYLAPOD 180
QY 121 DSATKTFPNNMENPWWKVDITIADESFSQVLDGRVVKINTEVRSFGPSRSGFYLAPOD 180
DB 121 DSATKTFPNNMENPWWKVDITIADESFSQVLDGRVVKINTEVRSFGPSRSGFYLAPOD 180
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DB 181 YGCGMSLIAVREYFRKCPRIIONGALFOETLSGAESTSLVAARSGCIANAEEVDVPIKLY 240
QY 241 CNGDGEWLPIGRMCKAGFEAVENGTVCRGCSGFFKANQGDPACTHCPINRRTISEGA 300
DB 241 CNGDGEWLPIGRMCKAGFEAVENGTVCRGCSGFFKANQGDPACTHCPINRRTISEGA 300
QY 301 TNCYCRNGYRADLDPLDMCTTIPSAPOAVISVNETSIEMETPPROSGGREDLVYNI 360
DB 301 TNCYCRNGYRADLDPLDMCTTIPSAPOAVISVNETSIEMETPPROSGGREDLVYNI 360
QY 361 ICKSCSGGRGACTRCGDNVQYAPROGLTEPRYIYIDLAAHQYTFEIOAVNGVTQDSPF 420
DB 361 ICKSCSGGRGACTRCGDNVQYAPROGLTEPRYIYIDLAAHQYTFEIOAVNGVTQDSPF 420
QY 421 SPQFASVNTTNOAPSAVSIMHOVSRFTVDSITLSMSQDPQNGVILDELYEKEISE 480
DB 421 SPQFASVNTTNOAPSAVSIMHOVSRFTVDSITLSMSQDPQNGVILDELYEKEISE 480
QY 481 YNAFAISPTNTVVOGLKAGAIYVPOVARTAVAGYGRYSGKXYPOTMTEAEYQTSIOEK 540
DB 481 YNAFAISPTNTVVOGLKAGAIYVPOVARTAVAGYGRYSGKXYPOTMTEAEYQTSIOEK 540
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DB 541 LPLIGSSAAGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHWTGPKKIYIDPF 600

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QY 721 IOLVGMRLGIAAGKYLADNMVYHRLDLAARNILVNSLVCKYDFGLSRFLIEDTSDPT 780
DB 721 IOLVGMRLGIAAGKYLADNMVYHRLDLAARNILVNSLVCKYDFGLSRFLIEDTSDPT 780
QY 781 TSALGCKTPIRWTAEALQYRKFTSASDVWSYGIWMVEWVSIGERPYMDNODVINAIE 840
DB 781 TSALGCKTPIRWTAEALQYRKFTSASDVWSYGIWMVEWVSIGERPYMDNODVINAIE 840
QY 841 QDYRLPPMDCPALHQLMLDCMKDRNHRPKFGQIVNTLDMKINENSLXAMAPLSGI 900
DB 841 QDYRLPPMDCPALHQLMLDCMKDRNHRPKFGQIVNTLDMKINENSLXAMAPLSGI 900
QY 901 NIPLDRTIPDYTSNTVDENLEAIKMGYKESFANAGFTSDVYSQMMEDILRLGVT 960
DB 901 NIPLDRTIPDYTSNTVDENLEAIKMGYKESFANAGFTSDVYSQMMEDILRLGVT 960
QY 961 AGHOKKILNSIOVMPAQNQIOSVE 985
DB 961 AGHOKKILNSIOVMPAQNQIOSVE 985

RESULT 3
AAB19590
ID AAB19590 standard; protein; 987 AA.
XX
AC AAB19590;
XX
XX 22-JAN-2001 ((first entry))
XX
DE Human CASB616.
XX
KM CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2V;
KM receptor protein tyrosine kinase; human; antigen; colon cancer;
XX ovary cancer; tumour; autoimmune disease; vaccine; therapy; diagnosis.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 568..569
FT /note="an additional Arg residue decodes from the
FT CASB616 nucleotide sequence given in the specification
FT (see AAB8548)", but is not given in the CASB616 amino
FT acid sequence in the specification"
FT Misc-difference 956
FT /note="encoded by GTT"
FT
XX
XX WO200053216-A2.
XX
XX 14-SEP-2000.
XX
XX 28-FEB-2000; 2000WO-EP001587.
XX
XX 05-MAR-1999; 99GB-00005124.
XX
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Vinals y De Baesolasc;
XX
XX WPI: 2000-587384/55.
XX
XX N-PSDB; AAB8548.
XX
XX Vaccine composition for treating ovarian and colon cancer, comprises
XX CASB616 polypeptides, polynucleotides or antigen presenting cells
XX expressing the polypeptides.
XX
```

```
PS Claim 1; Page 41; 57pp; English.
XX
XX The present sequence is that of human CASB616, a member of the EPH and
XX EPH-related family of receptor protein tyrosine kinases. CASB616 is also
XX known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2V. CASB616
XX polypeptides and polynucleotides are important immunogens for specific
XX prophylactic or therapeutic immunization against tumours, especially
XX colon cancer (claimed) and ovarian cancer. They are specifically
XX expressed or highly over-expressed in tumours compared to normal cells
XX and can thus be targeted by antigen-specific immune mechanisms leading to
XX destruction of the tumour cells. They can also be used to diagnose the
XX occurrence of tumour cells. Their inappropriate expression can also cause
XX an induction of autoimmune responses, which can be corrected through
XX vaccination using the CASB616 polypeptides or polynucleotides
XX
XX Sequence 987 AA.
XX
XX Query Match 99.8%; Score 5177.5; DB 3; Length 987;
XX Best Local Similarity 99.8%; Pired. No. 0;
XX Matches 986; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 MALRRGAAIILLPLAAVEETLMDSTTATAEIGMNVHPSPSGMEVSGYDENNTIRTYQ 60
DB 1 MALRRGAAIILLPLAAVEETLMDSTTATAEIGMNVHPSPSGMEVSGYDENNTIRTYQ 60
QY 61 VCNVFESSQNNWLRTKFIERRGAHRIHVENKFSYRDCSSIPSYVGSCKETFNLYYEADF 120
DB 61 VCNVFESSQNNWLRTKFIERRGAHRIHVENKFSYRDCSSIPSYVGSCKETFNLYYEADF 120
QY 121 DSATKTPNNMENNPNVAVDTIADDESFSQVDLGGKWKINTETVSRFGVPSRSGFYLAFO 180
DB 121 DSATKTPNNMENNPNVAVDTIADDESFSQVDLGGKWKINTETVSRFGVPSRSGFYLAFO 180
QY 121 DSATKTPNNMENNPNVAVDTIADDESFSQVDLGGKWKINTETVSRFGVPSRSGFYLAFO 180
DB 121 DSATKTPNNMENNPNVAVDTIADDESFSQVDLGGKWKINTETVSRFGVPSRSGFYLAFO 180
QY 181 YGCGMSLIAVRVFRKCPRIIONGAIPOELTSGAESTSLVAARGSCIANAEVDPILKY 240
DB 181 YGCGMSLIAVRVFRKCPRIIONGAIPOELTSGAESTSLVAARGSCIANAEVDPILKY 240
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QY 361 ICKSGSGRGACTRGNVQYAPRQLGTEPRYISDLAHTOYTFEIOAVNGVYTDOSP 420
DB 361 ICKSGSGRGACTRGNVQYAPRQLGTEPRYISDLAHTOYTFEIOAVNGVYTDOSP 420
QY 421 SPQASVNTTNOAAPSAVSIHQVSRVDSITLSWOPOPNPVILDYELQYKEKELSE 480
DB 421 SPQASVNTTNOAAPSAVSIHQVSRVDSITLSWOPOPNPVILDYELQYKEKELSE 480
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DB 481 YNATAIKSPNTTVVQGLKAGAIYFQVARTVAGYRSGKMYFQMTAEAYOTSIOEK 540
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DB 541 LPLIIGSSAAGLVFLIAVVAIYCN-RGFERADSEYTDLCQHYTSGHMPGKKIYDP 599
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DB 599 FTYEDPNEAVREPAKEIDISCVKIEOVIGAGEFGEVSGHKLPGKREIFAIAIKTLKSGY 659
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Db 901 INPLDLRTIPDTTSFNTVDEMELAKMGYKXSPNAGTSDVYSQMMEDILRLGYT 960  
QY 960 LAGHOKKILNSIQVRAQNNQIOSVEY 986  
Db 961 LAGHOKKILNSIQVRAQNNQIOSVEY 987

RESULT 4  
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ID AAW26366 standard; protein: 994 AA.  
XX  
AC AAW26366;  
XX  
DT 02-DEC-1997 (first entry)  
XX  
DE Mouse Nuk tyrosine kinase.  
XX  
XX Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction;  
XX axonogenesis; neurodegenerative disease; Alzheimer's disease;  
XX Parkinson's disease; Huntington's disease; multiple sclerosis;  
XX amyotrophic lateral sclerosis; Wernicke's disease; nerve damage; trauma;  
XX ischemia; stroke.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
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FT Protein /label= Sig\_peptide  
FT Domain /label= Mat\_protein  
FT Domain 27..548  
FT Region /label= Extracellular\_domain  
FT FT /label= FNIII  
FT FT /note= "fibronectin type III repeat"  
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FT FT /label= FNIII  
FT Domain /note= "fibronectin type III repeat"  
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FT FT /label= 575..994  
FT Region /label= Cytoplasmic\_domain  
FT FT /label= 623..888  
FT FT /label= Tyrosine-kinase\_region

MO9714966-A1.  
XX  
PD 24-APR-1997.  
XX  
EF 10-OCT-1996; 96WC-CA000679.  
XX  
PR 13-OCT-1995; 95US-0005518P.  
XX  
PA (MOUN) MOUNT SINAI HOSPITAL CORP.  
XX  
PI Pawsen A, Henkemeyer M;  
XX  
DR WPI; 1997-245245/22.  
XX  
XX N-PSDB; AAT84528.  
XX  
PT Activation of ligand regulatory pathways by Eph subfamily receptor  
PT tyrosine kinases - for stimulating or inhibiting axonogenesis, useful for  
PT treatment of e.g. neurodegenerative diseases such as Alzheimer's or

PT Parkinson's diseases.  
XX  
XX Disclosure; Fig 3; 55pp; English.  
XX  
XX Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine kinase  
CC that is essential for formation of the medial tract of the anterior  
CC commissure of the brain, and which appears to play a role in the  
CC formation of the habenular interpeduncle tract. Its amino acid sequence  
CC was deduced from cDNA clones (see A4784528) isolated from an embryo cDNA  
CC library. The extracellular domain of Nuk was shown to be sufficient for  
CC formation of the medial tract. Eph subfamily receptor tyrosine kinases  
CC (e.g. the Nuk extracellular domain) can be used in claimed methods to:  
CC activate a ligand regulatory pathway in a cell; identify substances able  
CC to bind a ligand for an Eph subfamily receptor tyrosine kinase; and to  
CC affect neuronal development or regeneration, especially the stimulation  
CC or inhibition of axonogenesis, in a mammal. Activation of the ligand  
CC regulatory pathway results in downstream activation of a series of  
CC regulatory pathways in cells that control gene expression, cell division,  
CC cytoskeletal architecture, cell metabolism, cell migration and cell-cell  
CC interactions. Substances which activate the ligand regulatory pathway may  
CC be used for stimulating or inhibiting neuronal development regeneration  
CC and axonal migration associated with neurodegenerative disease e.g.  
CC Alzheimer's, Parkinson's or Huntington's diseases, multiple sclerosis,  
CC amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's  
CC disease, peripheral nerve damage, trauma and ischaemia resulting from  
CC stroke  
XX  
SQ Sequence 994 AA:  
SQ  
Query Match 98.9%; Score 5130; DB 2; Length 994;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Db 18 LLLPLLAAYETLMDSTTAETAEIGMWVHPSPSGMEVSGYDEMNTIRTYOVNVPSSG 77  
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Db 78 NNNLRTKFIIRRGARHIVHMKFVSVDCCSIPSPSCKETENLYYYEADFDLATKTFPN 137  
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Db 138 MMENPMVKVDITIADESFSQVDIGGRVKINTEVRSPGVSRSRGLTAAODVGGCSLLA 197  
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QY 250 PIGRCMKAGFEAVENGIVRGCPSGTFKANGDEACTHCPINSRTSGAINVCVRNGY 309  
Db 258 PIGRCMKAGFEAVENGIVRGCPSGTFKANGDEACTHCPINSRTSGAINVCVRNGY 317  
QY 310 YRADLPLDMPCTTIPSAFOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGR 369  
Db 318 YRADLPLDMPCTTIPSAFOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGR 377  
QY 370 GACTRCGDNVOYAPROGLTEPRITYSDLLARTQYFEIOAVNGVTDOSFPSPASVNI 429  
Db 378 GACTRCGDNVOYAPROGLTEPRITYSDLLARTQYFEIOAVNGVTDOSFPSPASVNI 437  
QY 430 TTNGAAPSAVSIMHQSRTVDSITLSMSQPDNGVITLDELYOYEXKEISEVNAATKSP 489  
Db 438 TTNGAAPSAVSIMHQSRTVDSITLSMSQPDNGVITLDELYOYEXKEISEVNAATKSP 497  
QY 490 TMTVTVOGLKAGAIYFQVARTVAGYGRYSKMPQMTAEAYOTSIOEKPLIIGSSA 549  
Db 498 TMTVTVOGLKAGAIYFQVARTVAGYGRYSKMPQMTAEAYOTSIOEKPLIIGSSA 557  
QY 550 AGIVFLIAVVTAIVONRGRGFERADSEYDKIOHTSGMTSGMKIYIDPFYEEDPNEAV 609  
Db 558 AGIVFLIAVVTAIVONRGRGFERADSEYDKIOHTSGMTSGMKIYIDPFYEEDPNEAV 617

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QY 610 REFKEIDISCVKIEGVIGAGEFGEVCGSHLPLPKGRKEIFVAIKTLKSGYTEKQRDFLS 669
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Db 618 REFKEIDISCVKIEGVIGAGEFGEVCGSHLPLPKGRKEIFVAIKTLKSGYTEKQRDFLS 677
|
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QY 670 EASIMQGFPHPNVTHIEGVVTKSTPMTTTEMENENSLDSELRONDGGCTTVQLVGMKRG 729
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|
Db 678 EASIMQGFPHPNVTHIEGVVTKSTPMTTTEMENENSLDSELRONDGGCTTVQLVGMKRG 737
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QY 730 IAAGMKYLDANVYVHRDLAARNILVNSNLVCKVSPFGLSRPLEDDTSDPTYSALGKIP 789
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Db 738 IAAGMKYLDANVYVHRDLAARNILVNSNLVCKVSPFGLSRPLEDDTSDPTYSALGKIP 797
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QY 790 IEMTAPBEALQYRKFTSASDVMSYGIYMAEVMASGERPFDYDMTNQDYINAIEDDYRLPPPM 849
|
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|
Db 798 IEMTAPBEALQYRKFTSASDVMSYGIYMAEVMASGERPFDYDMTNQDYINAIEDDYRLPPPM 857
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QY 850 DCPSSALHQLMLDCMQKDRNHRPFQGIYNTLDMKIMNPNSLKAMPPLSSGILPLLDRTI 909
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Db 858 DCPSSALHQLMLDCMQKDRNHRPFQGIYNTLDMKIMNPNSLKAMPPLSSGILPLLDRTI 917
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QY 910 PDYTSFNTVDLWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTLAHHQKILIN 969
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Db 918 PDYTSFNTVDLWLEAIKMGQYKESFANAGFTSPDVVSQMMEDILRLGYTLAHHQKILIN 977
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QY 970 SIQWMAQNNQIOQSEV 986
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Db 978 SIQWMAQNNQIOQSEV 994
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RESULT 5
AAU01907
ID AAU01907 standard; protein; 994 AA.
XX
AC AAU01907;
XX
DT 29-AUG-2001 (first entry)
XX
DE Murine neural kinase (Nuk) polypeptide.
XX
XX
KM Neural kinase; Nuk; receptor tyrosine kinase; axonal migration; stroke;
KM nerve fibre; cell-cell interaction; axonogenesis; neuronal development;
KM regeneration; neurodegenerative disorder; Alzheimer's disease; ischaemia;
KM Parkinson's disease; Huntington's disease; demyelinating disease;
KM multiple sclerosis; amyotrophic lateral sclerosis; deficiency disease;
KM Wernicke's disease; nutritional polyneuropathy; multistem degeneration;
KM progressive supranuclear palsy; Shy Drager's syndrome; mouse;
KM olivoponto cerebellar atrophy; peripheral nerve damage.
XX
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..26 /note="Signal peptide"
FT 26..548 /note="Extracellular domain, preferably residues 26-544"
FT Domain
FT Protein
FT 27..994 /note="Mature murine neural kinase"
FT 52..119 /note="Ig-like domain"
FT Domain
FT 239..268 /note="Ig-like domain"
FT Region
FT 330..420 /note="Ig-like Nuk repeat"
FT Region
FT 444..534 /note="Fibronectin type III repeat"
FT Region
FT 549..574 /note="Fibronectin type III repeat"
FT Domain
FT 600..618 /note="Hydrophobic transmembrane domain"
FT Binding-site
FT 601..994 /note="SH2 domain binding site"
FT Region
FT 604 613 /note="Carboxy terminal"
FT Modified-site
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FT Domain 623..888
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|
FT Binding-site /note="Catalytic tyrosine kinase domain"
FT 623..707
|
|
|
FT /note="ATP binding site"
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US6218356-B1.
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PD 17-APR-2001.
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PR 13-OCT-1995; 95US-00542635.
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PR 29-APR-1994; 94US-00235407.
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PR 28-APR-1995; 95MO-CA000254.
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|
(MOUN ) MOUNT SINAI HOSPITAL CORP.
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Pawson A, Henkemeyer M, Letwin K;
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MPI; 2001-289845/30.
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|
DR N-PSDB; AAS03812.
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|
XX New composition comprising neural receptor tyrosine kinase protein useful
XX for inhibiting or stimulating axonogenesis, neuronal development, or
XX regeneration and axonal migration.
XX
XX Claim 1; Fig 2; 86pp; English.
XX
XX The sequence represents a mouse neural kinase (Nuk) polypeptide. The
XX murine Nuk locus has been mapped to the distal end of chromosome four.
XX The polypeptide is a novel receptor tyrosine kinase protein, and is found
XX to be expressed at high levels within migrating axons and is associated
XX with nerve fibres. It functions to regulate specific cell-cell
XX interactions during early development of the nervous system and in
XX axonogenesis. Substances which bind to the Nuk protein, particularly
XX ligands, may be used for stimulating or inhibiting neuronal development,
XX regeneration and axonal migration associated with neurodegenerative
XX disorders and conditions involving trauma and injury to the nervous
XX system. These disorders include Alzheimer's disease, Parkinson's disease,
XX Huntington's disease, demyelinating diseases such as Wernicke's
XX amyotrophic lateral sclerosis, deficiency diseases such as Shy Drager's
XX disease and nutritional polyneuropathy, progressive supranuclear palsy,
XX Shy Drager's syndrome, multistem degeneration, olivoponto cerebellar
XX atrophy, peripheral nerve damage, and ischaemia resulting from stroke.
XX The proteins may be used to prepare antibodies having specificity for Nuk
XX proteins, which can be used to diagnose or treat disorders of the nervous
XX system. These proteins are also used for screening agonists or
XX antagonists of the interactions of the Nuk proteins with binding
XX molecules
XX
XX
XX Sequence 994 AA;
XX
XX Query Match 98.9%; Score 5130; DB 4; Length 994;
XX Best Local Similarity 99.5%; Pred. No. 0;
XX Matches 972; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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Db 258 PIGRCMKAGFEAVENGTVGRGCPSCGTFKXANQDGEACTHCPINSRFTTSBGATNCVRNGY 317

Qy 310 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPRPDSGRDLVNIICKSCGSGR 369

Db 318 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPRPDSGRDLVNIICKSCGSGR 377

Qy 370 GACTRCGDNYQYAPROGLTEPRITISDLAHTQYFEIQAQVAVTIDQSFSPQFASVNI 429

Db 378 GACTRCGDNYQYAPROGLTEPRITISDLAHTQYFEIQAQVAVTIDQSFSPQFASVNI 437

Qy 430 TTNOAASANSINHQVSRITVDSITLSWSPDQNGVITLDELOYEKEISENNATIKSP 489

Db 438 TTNOAASANSINHQVSRITVDSITLSWSPDQNGVITLDELOYEKEISENNATIKSP 497

Qy 490 TMTVTGGLKAGAIYVQVARTVAGYGRYSGMYQTMTEARVYQSIQKPLIIGSSA 549

Db 498 TMTVTGGLKAGAIYVQVARTVAGYGRYSGMYQTMTEARVYQSIQKPLIIGSSA 557

Qy 550 AGVFLIAVVVIAIVCNRRGFERPADSEYTDKLOHYTSGMTPGMKIYIDPFYEDPNEAV 609

Db 558 AGVFLIAVVVIAIVCNRRGFERPADSEYTDKLOHYTSGMTPGMKIYIDPFYEDPNEAV 617

Qy 610 REPAKEIDISCVAIEQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDELS 669

Db 618 REPAKEIDISCVAIEQVIGAGEFGEVCSGHLKPGKREIFVAIKTLKSGYTEKORDELS 677

Qy 670 EASIMGQFDPHNYIHEGVVTKSTPVMIITEFMENGLSDSFLRQNDGQFTVIQVGMRLG 729

Db 678 EASIMGQFDPHNYIHEGVVTKSTPVMIITEFMENGLSDSFLRQNDGQFTVIQVGMRLG 737

Qy 730 IAGMKYLAQNYVHRRLAARNTLVNSNLVCKYSDGSLRFLDDPTSDPTYSALGKRP 789

Db 738 IAGMKYLAQNYVHRRLAARNTLVNSNLVCKYSDGSLRFLDDPTSDPTYSALGKRP 797

Qy 790 IRMTAPEALQYRKFTSASDVMSYGIWMEVMSYGERPYMDMTQDINAIEDYRLPPM 849

Db 798 IRMTAPEALQYRKFTSASDVMSYGIWMEVMSYGERPYMDMTQDINAIEDYRLPPM 857

Qy 850 DCSALHQLMDQWQDRNRHPRFGQIVTLDKINPNSIKRAMAPLSSGINVPLIDRTI 909

Db 858 DCSALHQLMDQWQDRNRHPRFGQIVTLDKINPNSIKRAMAPLSSGINVPLIDRTI 917

Qy 910 PDYTSFNTVDEMLAIKMGQYKESFANAGTSPDVVSQMMEDILALGTLAGHOKKILN 969

Db 918 PDYTSFNTVDEMLAIKMGQYKESFANAGTSPDVVSQMMEDILALGTLAGHOKKILN 977

Qy 970 SIQVRAQNNQIOSVEV 986

Db 978 SIQVRAQNNQIOSVEV 994

RESULT 6  
AAR87018  
ID AAR87018 standard; protein; 994 AA.  
XX  
AC AAR87018;  
XX  
DT 19-MAR-1996 (first entry)  
XX  
DE Receptor tyrosine kinase (neural kinase).  
XX  
KW Receptor tyrosine kinase; neural kinase; Nuk; axon; axonogenesis;  
XX  
OS nerve disorder.  
XX  
Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT 1.26  
FT /label= Sig\_peptide  
FT 27..548  
FT Region  
FT /label= Extracellular region  
FT /note= "the extracellular region (amino acids 27-548)  
FT includes an N-terminal Ig-like domain and an Ig-like Nuk

FT FT repeat"  
FT Region 330..420  
FT /label= FNIII  
FT /note= "fibronectin type III repeat"  
FT Region 444..534  
FT /label= FNIII  
FT /note= "fibronectin type III repeat"  
FT Region 549..574  
FT /label= Transmembrane\_region  
FT 575..994  
FT /label= Cytoplasmic\_region  
FT 623..707  
FT /label= Tyrosine-kinase\_catalytic\_domain  
FN W09530326-A1.  
XX 09-NOV-1995.  
PD 28-APR-1995; 95WD-CA000254.  
XX 29-APR-1994; 94US-00235407.  
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
XX Pawsom A, Henkemeyer M, Letwin K;  
XX WPI, 1995-393299/50.  
DR N-PSDB; AAT07308.  
XX DNA encoding neural receptor tyrosine kinase - useful in gene therapy of  
XX nerve disorders, and for diagnosis and identification of therapeutic  
XX agents.  
XX Claim 1; Page 70-74; 103pb; English.  
XX A novel receptor tyrosine kinase (AAR87018), designated neural kinase  
XX (Nuk) (AAR87018), is encoded by cDNA (AAT07308) obtd. from a mouse embryo  
XX library. Nuk is expressed in migrating axons and is involved in cell-cell  
XX interactions and axonogenesis in development of the nervous system. Nuk  
XX or its fragments (pref. amino acids 26-548 or 601-994) are used to  
XX identify (ant)agonists of the (activated) receptor tyrosine kinase as a  
XX means of treating nerve disorders and damage, or to raise antibodies used  
XX to monitor axon migration and nerve cell interactions  
XX Sequence 994 AA:  
SQ  
Query Match 98.8%; Score 5126; DB 2; Length 994;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 971; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
Qy 10 LLLPLLAAYBETLMDSTTATAEIGMMVHPSPSGMEVSGYDENMTIRTYQVGNVFESSQ 69  
Db 18 LLLPLLAAYBETLMDSTTATAEIGMMVHPSPSGMEVSGYDENMTIRTYQVGNVFESSQ 77  
Qy 70 NNMLRTKFIIRRGARHIVEMKFSVRDSSIPSPGSCKETENLYYYEADFDSATKTFPN 129  
Db 78 NNMLRTKFIIRRGARHIVEMKFSVRDSSIPSPGSCKETENLYYYEADFDSATKTFPN 137  
Qy 130 WMENPWYKVDITADSFQVDIGRYMKINTVRSRGPYSRSGFLYAFQDYGGCGLIA 189  
Db 138 WMENPWYKVDITADSFQVDIGRYMKINTVRSRGPYSRSGFLYAFQDYGGCGLIA 197  
Qy 190 VRVFRKCPRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYCNGDEMTLY 249  
Db 198 VRVFRKCPRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYCNGDEMTLY 257  
Qy 250 PIGRCMKAGFEAVENGTVGRGCPSCGTFKXANQDGEACTHCPINSRFTTSBGATNCVRNGY 309  
Db 258 PIGRCMKAGFEAVENGTVGRGCPSCGTFKXANQDGEACTHCPINSRFTTSBGATNCVRNGY 317  
Qy 310 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPRPDSGRDLVNIICKSCGSGR 369  
Db 318 YRADLDLDMPCCTTISAPQAVISSVNETSIMLEMPRPDSGRDLVNIICKSCGSGR 377

QY	370	GACRCDCDNQVAPRQGLTEPR	IYISDILLATQYTFELQAVNGVTDSPSPQFASVNI	428
Db	378	GACRCDCDNQVAPRQGLTEPR	IYISDILLATQYTFELQAVNGVTDSPSPQFASVNI	437
QY	430	TTTNOAASAVSINHQVSR	YDSTLTLSNSQDPDPNGVILDYELQYKEKLSYNTATLAKSP	488
Db	438	TTTNOAASAVSINHQVSR	YDSTLTLSNSQDPDPNGVILDYELQYKEKLSYNTATLAKSP	497
QY	490	TNTVTVGGLKAGAIYFQV	PARFVAGRGYSGKMTFQMTTEAEVYQTSIOEKLPLIGSSA	548
Db	498	TNTVTVGGLKAGAIYFQV	PARFVAGRGYSGKMTFQMTTEAEVYQTSIOEKLPLIGSSA	557
QY	550	AGLVELI	AVVIVAIIVCNRRGFESADSEYTDKIQHTYSGHMPQMKIYIDPTTYEDPNEAV	608
Db	558	AGLVELI	AVVIVAIIVCNRRGFESADSEYTDKIQHTYSGHMPQMKIYIDPTTYEDPNEAV	617
QY	610	REFAKEIDISCVKIEQV	IGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORPFLS	668
Db	618	REFAKEIDISCVKIEQV	IGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORPFLS	677
QY	670	EASIMGQFDPHPNVIH	LEGVTVKSTPVMITTEFMEKSLDSFLRQNDQGFVILQVGMRLG	728
Db	678	EASIMGQFDPHPNVIH	LEGVTVKSTPVMITTEFMEKSLDSFLRQNDQGFVILQVGMRLG	737
QY	730	IAAGMKRLAMNVVHHD	LAARNILVNSNLVCKVSPGLSRFLEDPTSDPYTSLAGKIP	788
Db	738	IAAGMKRLAMNVVHHD	LAARNILVNSNLVCKVSPGLSRFLEDPTSDPYTSLAGKIP	797
QY	790	IRMTAPALQYRKFTS	ASDVMSYGIYVMEVNSYGERPYWDTNODVINALFQDYRLPEPM	848
Db	798	IRMTAPALQYRKFTS	ASDVMSYGIYVMEVNSYGERPYWDTNODVINALFQDYRLPEPM	857
QY	850	DCPSALHQLMLDCQK	DRNHRPKFGQIVNTLDKMIRNPSILKAPAPLSSGILNPLDRTI	908
Db	858	DCPSALHQLMLDCQK	DRNHRPKFGQIVNTLDKMIRNPSILKAPAPLSSGILNPLDRTI	917
QY	910	PDYTSSENTVD	EWLEAIKMGQYKESFANAGFTSFYVVSQMMEDILRLGVTLAGHQKILN	968
Db	918	PDYTSSENTVD	EWLEAIKMGQYKESFANAGFTSFYVVSQMMEDILRLGVTLAGHQKILN	977
QY	970	SIQVMPRAQNNQIOSVEY	966	
Db	978	SIQVMPRAQNNQIOSVEY	994	
RESULT 7				
AAR85089				
ID	AAR85089	standard; protein; 970 AA.		
XX	AA85089;			
AC	16-APR-1996	(first entry)		
DT	EPH-like receptor protein tyrosine kinase HEK5.			
XX	human eph-like kinase; therapy; diagnosis; vector; antibody.			
KW	human eph-like kinase; therapy; diagnosis; vector; antibody.			
XX	human eph-like kinase; therapy; diagnosis; vector; antibody.			
OS	Homo sapiens.			
XX	MO528484-A1.			
FN	26-OCT-1995.			
PD	14-APR-1995;	95WC-US004681.		
XX	15-APR-1994;	94US-0022509.		
PR	(AMGE-) AMGEN INC.			
XX	Fox GM, Welch AA, Jing S;			
XX				

[illegible]



DT 25-MAR-2003 (revised)  
DT 11-NOV-1995 (first entry)  
XX Eph-related PTK Cdk5+.  
XX Cdk5+, Eph, protein tyrosine-kinase; PTK; cancer; diagnosis; prognosis.  
XX Gallus sp.  
XX MO9515375-A1.  
XX 08-JUN-1995.  
XX 07-SEP-1994; 94MO-US010140.  
XX 03-DEC-1993; 93US-00162809.  
XX (LJOL-) LA JOLIA CANCER RES FOUND.  
XX Pasquale EB, Sajjadi FG;  
XX WPI, 1995-215256/28.  
XX N-PSDB; AAQ90657.  
XX Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing  
PT cancer.  
XX Claim 11, Page 71-75; 129pp; English.  
XX A cDNA clone encoding a novel variant of Eph-related PTK Cdk5, Cdk5+  
CC (AAQ90657), was isolated from a chick embryo library in lambda g11.  
CC Cdk5+ protein (AA875709) contains a 16-amino acid insertion in the  
CC juxtamembrane domain, and be a result of alternative splicing. Cdk5+ is  
CC exclusively expressed in the CNS. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
XX Sequence 1011 AA;  
SQ

Query Match 95.8%; Score 4971.5; DB 2; Length 1011;  
Best Local Similarity 94.2%; Pred. No. 0;  
Matches 936; Conservative 29; Mismatches 12; Indels 17; Gaps 2;

QY 10 LLLPLLAEEITLMDSTTAELGMMVHPSPGMEVSGYDENMTIRTYQVCNPFSSQ 69  
DB 18 LALLPLLAEEITLMDSTTAELGMMVHPSPGMEVSGYDENMTIRTYQVCNPFSSQ 77  
QY 70 NMLRTKFIIRRGARHIVEMKFSVSDCSIPSPGCKETFNLYYYEADPDSATKTFPN 129  
DB 78 NMLRTKFIIRRGARHIVEMKFSVSDCSIPSPGCKETFNLYYYEADPDSATKTFPN 137  
QY 130 WMENPWKVDITIADESFQVDLGRVWKINTEVRSPGYSRSGFYLAQDYGGMSLIA 189  
DB 138 WMENPWKVDITIADESFQVDLGRVWKINTEVRSPGYSRSGFYLAQDYGGMSLIA 197  
QY 190 VRFVYRCPRIIONGAFQETLSGABESTLVAARGSCIANAEVDVPIKLYCNGDEMLV 249  
DB 198 VRFVYRCPRIIONGAFQETLSGABESTLVAARGSCIANAEVDVPIKLYCNGDEMLV 257  
QY 250 PISGCMKAGFEAVENGTVGRGCPSTGTFKANOGDEACTHCPINSRTTSEGATNCVRNGY 309  
DB 258 PISGCMKAGFEAVENGTVGRGCPSTGTFKANOGDEACTHCPINSRTTSEGATNCVRNGY 317  
QY 310 YRADLDELDPCTTIPAPAVISSVNETSLMLEMTPPRDSGREDLVNIIKSCGSGR 369  
DB 318 YRADLDELDPCTTIPAPAVISSVNETSLMLEMTPPRDSGREDLVNIIKSCGSGR 377  
QY 370 GACTRCGDNTQYAFRCGLTEPRYISDLLAHQYTFEIQAVNGVTDQSPFSPQFASVNI 429  
DB 378 GACTRCGDNTQYAFRCGLTEPRYISDLLAHQYTFEIQAVNGVTDQSPFSPQFASVNI 437  
QY 430 TTNOAPSAVSIHQVSRVYDSTLTSWSQPDQPNGLVDYELQYKEKLSVNAIAIKSP 489  
DB 438 TTNOAPSAVSIHQVSRVYDSTLTSWSQPDQPNGLVDYELQYKEKLSVNAIAIKSP 497

QY 490 TINTVVOGLKAGATVYQVARTVAGYGRYSKKYFQTMTEAEYQTSIOEKLPIIGSSA 549  
DB 498 TINTVVOGLKAGATVYQVARTVAGYGRYSKKYFQTMTEAEYQTSIOEKLPIIGSSA 557  
QY 550 AGLVFLIAVAVIAIVCN-RSGFERADSEYTDKOHYTSGH-----MTPG 592  
DB 558 AGLVFLIAVAVIIIVCNRRRGFERADSEYTDKOHYTSGHSTYGPPLGVRSLFPTPG 617  
QY 593 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQYIAGFEGEVCSGHLKPGKEIFVAI 652  
DB 618 MKIYIDPFTYEDPNEAVREFAKEIDISCVKIEQYIAGFEGEVCSGHLKPGKEIFVAI 677  
QY 653 KTLKSGYTEKORRDPFLSEASIMGOFDHPNVIHLEGVTKSTPPVITTEPMENSLDSFLR 712  
DB 678 KTLKSGYTEKORRDPFLSEASIMGOFDHPNVIHLEGVTKSTPPVITTEPMENSLDSFLR 737  
QY 713 QNDGQFTVIOVGMRLGIAAGMKYIADMNYYHRDLAARNIIVNSNLVCKVSDFGLSRFL 772  
DB 728 QNDGQFTVIOVGMRLGIAAGMKYIADMNYYHRDLAARNIIVNSNLVCKVSDFGLSRFL 797  
QY 773 DDTSDPTYSALGKIPRMTAPALIOYRKFTSADVWSYGIWMEVWSYGERPYMDNTN 832  
DB 798 DDTSDPTYSALGKIPRMTAPALIOYRKFTSADVWSYGIWMEVWSYGERPYMDNTN 857  
QY 833 QDVINAIHQDYRLPFPMDCPALHQLMLDCWQKXDRNHRPKFGQIVNTLDKXIRNPNLSIKA 892  
DB 858 QDVINAIHQDYRLPFPMDCPALHQLMLDCWQKXDRNHRPKFGQIVNTLDKXIRNPNLSIKA 917  
QY 893 MAPLSSGINTLPLDRTIPDYTSFNTVDENLEAIKMGQYKESFANAAGTSFENVQMMED 952  
DB 918 MAPLSSGINTLPLDRTIPDYTSFNTVDENLEAIKMGQYKESFANAAGTSFENVQMMED 977  
QY 953 ILRLGVTLAGHQKILNSIQVRAQMNQIQSVEV 986  
DB 978 ILRLGVTLAGHQKILNSIQVRAQMNQIQSVEV 1011

Search completed: August 28, 2004, 04:08:44  
Job time : 100.585 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:54 ; Search time 19.6423 Seconds

(without alignments)  
2796.715 Million cell updates/sec

Title: US-09-914-883-4

Perfect score: 5571

Sequence: 1 MALRRIGALLPLLAAYE.....QGIFKEDSHKSNDCGCG 1055

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1 5568 99.9 1055 1 EPHB2\_HUMAN P29323 homo sapien

2 5129 92.1 994 1 EPHB2\_MOUSE P54763 mus musculi

ALIGNMENTS

RESULT 1

EPHB2\_HUMAN

ID EPHB2\_HUMAN STANDARD; PRT; 1055 AA.

AC P29323; 043477;

DT 01-DEC-1992 (Rel. 24, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein

kinase receptor EPH-3) (DRT) (Receptor protein-tyrosine kinase HEK5

(ERK)).

GN EPHB2 OR EPH3 OR ERK OR DRT OR HEK5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI\_TaxID=9606;

OC [1]

OC SEQUENCE FROM N.A. (ISOFORM SHORT).

OC TISSUE=Fetal brain;

OC MEDLINE=96154673; PubMed=8589679;

OC Ikegaki N., Tang X.X., Liu X.-G., Biegel J.A., Allen C.,

OC Yoshida A., Sultan E.P., Brodeur G.M., Pleasure D.B.;

OC "Molecular characterization and chromosomal localization of DRT

OC (EPH3): a developmentally regulated human protein-tyrosine kinase

OC gene of the EPH family.";

OC Hum. Mol. Genet. 4:2033-2045(1995).

OC [2]

RP SEQUENCE FROM N.A. (ISOFORM SHORT).

RC TISSUE=Gastric carcinoma;

RA MEDLINE=93343925; PubMed=7688222;

RT Iwase T., Tanaka M., Suzuki M., Naito Y., Sugimura H., Kino I.;

RT "Identification of protein-tyrosine kinase genes preferentially

RT expressed in embryo stomach and gastric cancer.";

RL Biochem. Biophys. Res. Commun. 194:598-705(1993).

RC [3]

RP SEQUENCE FROM N.A. (ISOFORM LONG).

RC TISSUE=Fetal brain;

RA MEDLINE=98359217; PubMed=9696046;

RT Tang X.X., Pleasure D.B., Brodeur G.M., Ikegaki N.;

RT "A variant transcript encoding an isoform of the human protein

RT tyrosine kinase EPHB2 is generated by alternative splicing and

RT alternative use of polyadenylation signals.";

RL Oncogene 17:521-526(1998).

RC [4]

RP SEQUENCE OF 15-986 FROM N.A. (ISOFORM SHORT).

RC TISSUE=Brain;

RA MEDLINE=95206782; PubMed=7898931;

RT Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,

RT Basu R., Welcher A.A.;

RT "cDNA cloning and tissue distribution of five human EPH-like receptor

RT protein-tyrosine kinases.";

RL Oncogene 10:897-905(1995).

RC [5]

RP SEQUENCE OF 509-986 FROM N.A. (ISOFORM SHORT).

RC TISSUE=Brain;

RA Saito T., Naochiko S., Kitahara M., Murata M., Yamamoto Y.,

RT Hori T., Matsuda Y.;

RT Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.

RL [6]

RP SEQUENCE OF 652-712 FROM N.A.

RA MEDLINE=91296584; PubMed=1648701;

RT Chan J., Watt V.M.;

RT "week and erk, new members of the eph subclass of receptor protein-

RT tyrosine kinases.";

RL Oncogene 6:1057-1061(1991).

RC [7]

RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF 910-986 (ISOFORM SHORT).

RA MEDLINE=99132419; PubMed=9933164;

RT Thanos C.D., Goodwill K.E., Bowie J.U.;

RT "Oligomeric structure of the human EphB2 receptor SAM domain.";

RL Science 283:833-836(1999).

CC -1- FUNCTION: Receptor for members of the ephrin-B family.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.

CC -1- SUBUNIT: The ligand-activated form interacts with multiple

CC proteins, including Grb2-activating protein (RASGAP) through its

CC SH2 domain. Binds RASGAP through the juxtamembrane tyrosines

CC residues. Interacts with PRKCBP (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=Long; Synonyms=EPHB2V;

CC IsoId=P29323-1; Sequence=Displayed.

CC Name=Short;

CC IsoId=P29323-2; Sequence=VSP\_003016, VSP\_003017;

CC -1- TISSUE SPECIFICITY: Brain, heart, lung, kidney, placenta,

CC pancreas, liver and skeletal muscle. Preferentially expressed in

CC fetal brain.

CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.

CC -1- SIMILARITY: Contains 2 fibronectin type III domains.

CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin

CC receptor subfamily.

CC -----

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CC -----  
 EMBL; L41939; AAA99310.1; -  
 DR EMBL; D31661; BAA0506.1; -  
 DR EMBL; AF025304; AAB84602.1; -  
 DR EMBL; D14717; BAA03537.1; -  
 DR EMBL; L36643; AAB74244.1; -  
 DR EMBL; D37827; BAA07073.1; -  
 DR EMBL; X59292; CAA1981.1; -  
 DR PIR; A57174; A57174.  
 DR PDB; 1BAF; 15-FEB-99.  
 DR PDB; 1FOV; 04-JUL-00.  
 DR Genew; HXNC3393; EPHB2.  
 DR MIM; 600997; -  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 DR InterPro; IPR006209; EGF-like  
 DR InterPro; IPR001090; Ephrin\_receptor.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003962; FNIII subd.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001650; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase\_AS.  
 DR InterPro; IPR01426; Ykase\_receptor.  
 DR Pfam; PF00041; fn3\_2.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00014; FNTPRIT.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; Eph\_lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TYKIC; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR TYR KIN V.1; 1.  
 DR PROSITE; PS00791; RECEPTOR TYR KIN V.2; 1.  
 DR PROSITE; PS0105; SAM DOMAIN; 1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; 3d-structure;  
 KW Alternative splicing; Repeat.  
 FT SIGNAL 1  
 FT CHAIN 19 1055  
 FT DOMAIN 19 543  
 FT TRANSMEM 544 564  
 FT DOMAIN 565 1055  
 FT DOMAIN 184 324  
 FT DOMAIN 325 418  
 FT DOMAIN 436 520  
 FT DOMAIN 621 884  
 FT DOMAIN 913 977  
 FT SITE 984 986  
 FT NE\_BIND 627 635  
 FT BINDING 653 653  
 FT ACT\_SITE 746 746  
 FT MOD\_RES 596 596  
 FT MOD\_RES 602 602  
 FT MOD\_RES 780 780  
 FT MOD\_RES 930 930  
 FT CARBOHYD 265 265  
 FT CARBOHYD 336 336  
 FT CARBOHYD 428 428  
 FT CARBOHYD 482 482

FT VARSPPLIC 986 986 G -> V (in isoform Short).  
 FT VARSPPLIC 987 1055 /FtId=VSP\_003016.  
 FT VARSPPLIC 987 1055 Missing (in isoform Short).  
 FT VARSPPLIC 987 1055 /FtId=VSP\_003017.  
 FT VARIANT 671 671 A -> R.  
 FT VARIANT 671 671 /FtId=VAR\_004162.  
 FT CONFLICT 1 20 MALRGLGALLLLLAAVE -> MNPVIALPVCTYA  
 FT CONFLICT 1 20 (in REF. 2).  
 FT CONFLICT 154 154 G -> D (in REF. 2).  
 FT CONFLICT 476 476 K -> KO (in REF. 2).  
 FT CONFLICT 495 496 MISSING (in REF. 4).  
 FT CONFLICT 532 532 E -> D (in REF. 2).  
 FT CONFLICT 532 532 R -> RR (in REF. 1).  
 FT CONFLICT 568 568 M -> I (in REF. 4).  
 FT CONFLICT 589 589 I -> F (in REF. 4).  
 FT CONFLICT 788 788 S -> A (in REF. 2 AND 5).  
 FT CONFLICT 853 853 E -> K (in REF. 2 AND 5).  
 FT CONFLICT 923 923 L -> V (in REF. 3).  
 FT CONFLICT 956 956 V -> L (in REF. 1).  
 FT CONFLICT 958 958  
 FT CONFLICT 918 924  
 FT HELIX 925 926  
 FT TURN 928 930  
 FT HELIX 931 936  
 FT TURN 937 938  
 FT TURN 942 945  
 FT TURN 946 947  
 FT HELIX 950 956  
 FT TURN 957 957  
 FT HELIX 961 984  
 SQ SEQUENCE 1055 AA; 117506 MW; D0AA2CC8E6CDB8 CRC64;  
 Query Match 99.9%; Score 5568; DB 1; Length 1055;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1054; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALRGLGALLLLLAAVESTLMDSTTATATAGMVMVPPSGMEVSGYDENMNTIRTYQ 60  
 DB 1 MALRGLGALLLLLAAVESTLMDSTTATATAGMVMVPPSGMEVSGYDENMNTIRTYQ 60  
 QY 61 VCNVPESQNNWLTFTKTRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYEADP 120  
 DB 61 VCNVPESQNNWLTFTKTRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYEADP 120  
 QY 61 VCNVPESQNNWLTFTKTRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYEADP 120  
 DB 61 VCNVPESQNNWLTFTKTRRGARHIVEMKFSYRDCSSIPSPGCKETFNLYEADP 120  
 QY 121 DSAKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRGTAFOD 180  
 DB 121 DSAKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRGTAFOD 180  
 QY 121 DSAKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRGTAFOD 180  
 DB 121 DSAKTPNNMNMENWVVDITIADESFSQVDLGRVWKINTEVRSFPGVRSRGTAFOD 180  
 QY 181 YGCGMSLIAVVFYKCPRIIIONGAIPOETLSCAESTSLVAARGSCIANAEVDVPILKY 240  
 DB 181 YGCGMSLIAVVFYKCPRIIIONGAIPOETLSCAESTSLVAARGSCIANAEVDVPILKY 240  
 QY 241 CNGGEMLVPIGRCMCKAGFEAVENGTVCGCPGTGKANOGEACTHCINSRTSEGA 300  
 DB 241 CNGGEMLVPIGRCMCKAGFEAVENGTVCGCPGTGKANOGEACTHCINSRTSEGA 300  
 QY 241 CNGGEMLVPIGRCMCKAGFEAVENGTVCGCPGTGKANOGEACTHCINSRTSEGA 300  
 DB 241 CNGGEMLVPIGRCMCKAGFEAVENGTVCGCPGTGKANOGEACTHCINSRTSEGA 300  
 QY 301 TNCVCRNGYRADLDPLDMECTTIPSAPOAVISSVNETSLMLWTPEPRDSGREDLVYNI 360  
 DB 301 TNCVCRNGYRADLDPLDMECTTIPSAPOAVISSVNETSLMLWTPEPRDSGREDLVYNI 360  
 QY 301 TNCVCRNGYRADLDPLDMECTTIPSAPOAVISSVNETSLMLWTPEPRDSGREDLVYNI 360  
 DB 301 TNCVCRNGYRADLDPLDMECTTIPSAPOAVISSVNETSLMLWTPEPRDSGREDLVYNI 360  
 QY 361 ICKSCGSGRACRCGNNVOYARQGLTEPRITISLHAHTQYTBIAQVNVGTQSPF 420  
 DB 361 ICKSCGSGRACRCGNNVOYARQGLTEPRITISLHAHTQYTBIAQVNVGTQSPF 420  
 QY 361 ICKSCGSGRACRCGNNVOYARQGLTEPRITISLHAHTQYTBIAQVNVGTQSPF 420  
 DB 361 ICKSCGSGRACRCGNNVOYARQGLTEPRITISLHAHTQYTBIAQVNVGTQSPF 420  
 QY 421 SPQASVNTITNQAAPAVSIMHQSRTVDSITLSMQPQPPAGVILDELYEKELESE 480  
 DB 421 SPQASVNTITNQAAPAVSIMHQSRTVDSITLSMQPQPPAGVILDELYEKELESE 480  
 QY 421 SPQASVNTITNQAAPAVSIMHQSRTVDSITLSMQPQPPAGVILDELYEKELESE 480  
 DB 421 SPQASVNTITNQAAPAVSIMHQSRTVDSITLSMQPQPPAGVILDELYEKELESE 480  
 QY 481 YNATAISPNTYTVQGLKAGAIYVQVRAETVAGIGRYSGKMYFQTMBAEYQTSIQEK 540  
 DB 481 YNATAISPNTYTVQGLKAGAIYVQVRAETVAGIGRYSGKMYFQTMBAEYQTSIQEK 540  
 QY 541 LPLIGSSAGVFLIAVVTVAIVCNRRGERADSEYTDPLQYTGSHMTGPKIYIDPF 600  
 DB 541 LPLIGSSAGVFLIAVVTVAIVCNRRGERADSEYTDPLQYTGSHMTGPKIYIDPF 600

Db 541 LPLIGSSAAGVLLAVVIAIVCNRRGERADSEVTDKLOHYTSGHMTGPKKIYIDPF 600  
 QY 601 TYEDENAVAEFAKEIDISCVKIEQVIGAGEFGEVSCGHLKPKREIFAIAIKTLKSGYT 660  
 Db 601 TYEDENAVAEFAKEIDISCVKIEQVIGAGEFGEVSCGHLKPKREIFAIAIKTLKSGYT 660  
 QY 661 EKQRDPFLSASIMGQFDHPNVTHLEGVYKSTPVMITTEFMENGSLDSFLRQNDQFTV 720  
 Db 661 EKQRDPFLSASIMGQFDHPNVTHLEGVYKSTPVMITTEFMENGSLDSFLRQNDQFTV 720  
 QY 721 IOLVGMRLGIAAGMKYIADNNVYHRDLAARNILVNSLVCKVSDPGLSRPLEDDTSDPY 780  
 Db 721 IOLVGMRLGIAAGMKYIADNNVYHRDLAARNILVNSLVCKVSDPGLSRPLEDDTSDPY 780  
 QY 781 TSAAGKIPIRMTAPEAIOYRKFTSASDVMSYGIWMEVMSYGERPYMDTNDQVINAIE 840  
 Db 781 TSAAGKIPIRMTAPEAIOYRKFTSASDVMSYGIWMEVMSYGERPYMDTNDQVINAIE 840  
 QY 841 QDRLPFPNDCPSALHQMIDCWOKDRNHRPKFGQIVNTLDKIRPNLSIKAAPISSGI 900  
 Db 841 QDRLPFPNDCPSALHQMIDCWOKDRNHRPKFGQIVNTLDKIRPNLSIKAAPISSGI 900  
 QY 901 NLPLDRTIPDYTSFNTVDEMLAIKMGQKESFANAGFTSPDVASQMMMEDILRIGVTL 960  
 Db 901 NLPLDRTIPDYTSFNTVDEMLAIKMGQKESFANAGFTSPDVASQMMMEDILRIGVTL 960  
 QY 961 AGHQKILINSIQVRAQMOQIOSEVQPLARRPRATGRTKRCOPRDVYKTCNSNDGKK 1020  
 Db 961 AGHQKILINSIQVRAQMOQIOSEVQPLARRPRATGRTKRCOPRDVYKTCNSNDGKK 1020  
 QY 1021 GMGKKTDPGRGREIOGIFPKESHKESNDSCGCG 1055  
 Db 1021 GMGKKTDPGRGREIOGIFPKESHKESNDSCGCG 1055

RT orientation of longitudinally projecting axons.";  
 RL Development 127:1397-1410(2000).  
 RN [4]  
 RP INTERACTION WITH PRKCABP.  
 RX MEDLINE=99098206; PubMed=9883737;  
 RA Torres R., Firestein B.U., Dong H., Staudinger J., Olson E.N.,  
 RA Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.;  
 RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph  
 RT receptors and their ephrin ligands".  
 RL Neuron 21:1453-1463(1998).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 29-204.  
 RX MEDLINE=99068648; PubMed=9853759;  
 RA Himanen J.-P., Henkemeyer M., Nikolov D.B.;  
 RT "Crystal structure of the ligand-binding domain of the receptor  
 RT tyrosine kinase EphA2".  
 RL Nature 396:486-491(1998).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 29-208 IN COMPLEX WITH  
 RP EPHRIN-B2.  
 RX MEDLINE=21639766; PubMed=11780069;  
 RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,  
 RA Henkemeyer M., Nikolov D.B.;  
 RT "Crystal structure of an Eph receptor-ephrin complex".  
 RL Nature 414:933-938(2001).  
 CC -1- FUNCTION: Receptor for members of the ephrin-B family. Can  
 CC function in aspects of retinal ganglion cell axon guidance to the  
 CC optic disk even lacking its tyrosine kinase domain.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: Interacts with PRKCABP. The ligand-activated form  
 CC interacts with multiple proteins, including GTPase-activating  
 CC protein (RASAP) through its SH2 domain. Binds RASGAP through the  
 CC juxtamembrane tyrosine residues. Interacts with PRKCABP (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in cells of the developing outer  
 CC retina.  
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin  
 CC receptor subfamily.  
 CC -----  
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 CC -----  
 DR EMBL, L25690; AA472411.1; ALT\_INIT.  
 DR EMBL, X76011; CA53598.1; -.  
 DR PDB: 1NGY; 28-MAY-02.  
 DR PDB: 1NUR; 13-OCT-99.  
 DR MGD: MGI:99611; Ephd2.  
 DR GO: GO:0008046; F:axon guidance receptor activity; IDA.  
 DR GO: GO:0007411; P:axon guidance; IDA.  
 DR InterPro: IPR006209; EGF-like.  
 DR InterPro: IPR001090; Ephrin-receptor.  
 DR InterPro: IPR008957; FN-III-like.  
 DR InterPro: IPR003961; FN-III.  
 DR InterPro: IPR003962; FNIII subd.  
 DR InterPro: IPR008979; Gal bind-like.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR001660; SAM.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR InterPro: IPR008265; Tyr\_kinase\_AS.  
 DR InterPro: IPR001426; YKase\_receptorV.  
 DR Pfam: PF01404; Eph\_1bd; 1.  
 DR Pfam: PF00041; fn3; 2.  
 DR Pfam: PF00069; kinase; 1.  
 DR Pfam: PF00536; SAM; 1.

RESULT 2  
 EPR2\_MOUSE STANDARD; PRT; 994 AA.  
 ID EPR2\_MOUSE  
 AC P54763; O62213; Q9QVY4;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ephrin type-B receptor 2 precursor (EC 2.7.1.112) (Tyrosine-protein  
 DE kinase receptor Eph-3) (Neural kinase) (Nuk receptor tyrosine kinase)  
 DE (SEK-3).  
 GN EPHB2 OR EPH3 OR NUK OR SEK3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94181250; PubMed=8134103;  
 RA Henkemeyer M., Mategere L.E., McGlade J., Olivier J.P., Conlon R.A.,  
 RA Holmgaard D.P., Letwin K., Pawson T.;  
 RT "Immunolocalization of the Nuk receptor tyrosine kinase suggests roles  
 RT in segmental patterning of the brain and axonogenesis".  
 RL Oncogene 9:1001-1014(1994).  
 RN [2]  
 RP SEQUENCE OF 516-994 FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Brain;  
 RX MEDLINE=95034306; PubMed=7947319;  
 RA Becker N., Seltanidou T., Murphy P., Mattei M.-G., Topilko P.,  
 RA Nieto A., Wilkinson D.G., Charney P., Gilarde P.;  
 RT "Several receptor tyrosine kinase genes of the Eph family are  
 RT segmentally expressed in the developing hindbrain".  
 RL Mech. Dev. 47:3-17(1994).  
 RN [3]  
 RP FUNCTION:  
 RX MEDLINE=20171264; PubMed=10704386;  
 RA Mondal R., Wideman C., Kaprielian Z.;  
 RT "Complementary expression of transmembrane ephrins and their receptors  
 RT in the mouse spinal cord: a possible role in constraining the

DR PRINTS; PRO0014; FNTYPEIII.  
 DR PRINTS; PRO0109; TYRKINASE.  
 DR Prodom; PD001495; Ephrin\_receptor; 1.  
 DR Prodom; PD001001; Proc\_kinase; 1.  
 DR SMART; SM00615; Eph\_Lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00454; SAM; 1.  
 DR SMART; SM00219; TykC; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS01107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
 DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 DR PROSITE; PS01105; SAM DOMAIN; 1.  
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3d-structure.  
 FT SIGNAL; 1; 26  
 FT CHAIN; 27; 994  
 FT DOMAIN; 27; 551  
 FT TRANSMEM; 552; 572  
 FT DOMAIN; 573; 994  
 FT DOMAIN; 192; 329  
 FT DOMAIN; 330; 439  
 FT DOMAIN; 440; 537  
 FT DOMAIN; 629; 892  
 FT DOMAIN; 921; 985  
 FT SITE; 992; 994  
 FT NP\_BIND; 635; 643  
 FT BINDING; 661; 661  
 FT ACT\_SITE; 754; 754  
 FT MOD\_RES; 604; 604  
 FT MOD\_RES; 610; 610  
 FT MOD\_RES; 788; 788  
 FT MOD\_RES; 938; 938  
 FT DISULFID; 70; 192  
 FT DISULFID; 105; 115  
 FT CARBOHYD; 273; 273  
 FT CARBOHYD; 344; 344  
 FT CARBOHYD; 436; 436  
 FT CARBOHYD; 490; 490  
 FT CONFLICT; 576; 576  
 SQ SEQUENCE 994 AA; 110759 MW; BC6B9B12A070394C CRC64;

Query Match 92.1%; Score 5129; DB 1; Length 994;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-314;  
 Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LLLPLLAAYEETLMDSTATAELGMMVHPDPSGMEVSGYDENMNTIRIYQVCNVESSQ 69  
 DB 18 LLLPLLAAYEETLMDSTATAELGMMVHPDPSGMEVSGYDENMNTIRIYQVCNVESSQ 77

QY 70 NNMIRTFPIRRRGHRIHVEKFSVRCSSIPSPVPSCKETFNLYYYEADFDSATKTFPN 129  
 DB 78 NNMIRTFPIRRRGHRIHVEKFSVRCSSIPSPVPSCKETFNLYYYEADFDLATKTFPN 137

QY 130 WMENPMVKVDITIADESFSQVDLGRVMKINTEVRSFGPVRSGFYLAFODYGCMSLIA 189  
 DB 138 WMENPMVKVDITIADESFSQVDLGRVMKINTEVRSFGPVRSGFYLAFODYGCMSLIA 197

QY 190 VRVYRKCPRIIQNGAIFQETLSGAEISTVAARGSCIANAEVDVPILKYCNGDEMLV 249  
 DB 198 VRVYRKCPRIIQNGAIFQETLSGAEISTVAARGSCIANAEVDVPILKYCNGDEMLV 257

QY 250 PIGRCMKAGBEAVENTGVRGCPGTFKANOGEACTHCPINSRTSSECATVCVRNGY 309  
 DB 258 PIGRCMKAGBEAVENTGVRGCPGTFKANOGEACTHCPINSRTSSECATVCVRNGY 317

QY 310 YRADLDLDPCTTIPSAPOAVISVNETSLMLWTPPRDSGREDLVNIIICKSGSGR 369  
 DB 318 YRADLDLDPCTTIPSAPOAVISVNETSLMLWTPPRDSGREDLVNIIICKSGSGR 377

QY 370 GACTRCGDNVQYARQGLTEPRRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 429

DB 378 GACTRCGDNVQYARQGLTEPRRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNI 437  
 QY 430 TTNOAPASVIMQOVARTVDSITLSWSOPDPQPGVILDELOYEKELESEYNATAIKSP 489  
 DB 438 TTNOAPASVIMQOVARTVDSITLSWSOPDPQPGVILDELOYEKELESEYNATAIKSP 497

QY 490 TINTVVOGLKAGALVYQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKLPIIGSSA 549  
 DB 498 TINTVVOGLKAGALVYQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKLPIIGSSA 557

QY 550 AGLVFLAVVIALVCRNRFGRADSEYTKLQHYTSGHMTPGKIIYIDPFTYDPNEAV 609  
 DB 558 AGLVFLAVVIALVCRNRFGRADSEYTKLQHYTSGHMTPGKIIYIDPFTYDPNEAV 617

QY 610 REPAKEIDISCVKIEQVIGAGEFGEVCSGHUKLPGKKEIFVAIXTLKSGYTEKQRDFLS 669  
 DB 618 REPAKEIDISCVKIEQVIGAGEFGEVCSGHUKLPGKKEIFVAIXTLKSGYTEKQRDFLS 677

QY 670 EASIMGQPDHNVNHLGCVTKSTPVMITTEFMENGLSDSFLRNDQGFVIOQVGLRG 729  
 DB 678 EASIMGQPDHNVNHLGCVTKSTPVMITTEFMENGLSDSFLRNDQGFVIOQVGLRG 737

QY 730 IAGMKYLDADNVYHRDLAARNILVNSNLVCKVSDFLSFLBEDDTSDDPTYSALGKIP 789  
 DB 738 IAGMKYLDADNVYHRDLAARNILVNSNLVCKVSDFLSFLBEDDTSDDPTYSALGKIP 797

QY 790 IRMTAPEALIQYRKTSASDVWSYGIVMVEVNSYGERPYWMTNODVINAIEQDRLPPPM 849  
 DB 798 IRMTAPEALIQYRKTSASDVWSYGIVMVEVNSYGERPYWMTNODVINAIEQDRLPPPM 857

QY 850 DCPGSLHQLMDCQKCRNHRPKFGQIVNTLDKMRPNPSLKAPAPLSSGINLPILDRTI 909  
 DB 858 DCPGSLHQLMDCQKCRNHRPKFGQIVNTLDKMRPNPSLKAPAPLSSGINLPILDRTI 917

QY 910 PDYTSFNTVDEMLAIRMGOYKESFANAGFTSPDVVSQMMMEDILRVGVTLAHOXKILN 969  
 DB 918 PDYTSFNTVDEMLAIRMGOYKESFANAGFTSPDVVSQMMMEDILRVGVTLAHOXKILN 977

QY 970 SIQVRAQMNQIOSVE 985  
 DB 978 SIQVRAQMNQIOSVE 993

Search completed: August 28, 2004, 04:09:27  
 Job time : 20.6423 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:02:25 ; Search time 34.1156 Seconds

(without alignments)  
2974.650 Million cell updates/sec

Title: US-09-914-883-4

Perfect score: 5571  
Sequence: 1 MLRLRLGALLLLPLLAAYE.....QGIFKEDSHKESNDCSCG 1055

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%  
Maximum Match 100%

Listing first 45 summaries

Database: PIR.78:\*

1: PIR1:.\*  
2: PIR2:.\*  
3: PIR3:.\*  
4: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5088	91.3	970	2 178842	receptor protein-t

ALIGNMENTS

RESULT 1

178842 receptor protein-tyrosine kinase - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #ext\_change 18-Jun-1999

C/Accession: 178842

R/Fox, G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Weicher, Oncogene 10, 897-905, 1995

A/Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty

A/Reference number: 158351, MIMD:95206782; PMID:7898931

A/Accession: 178842

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-970 <RES>

A/Cross-references: GB:136643; NID:9551609; PIDN:AAV4244.1; PID:9551610

C/Genetics:

A/Genes: HK5

C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

F:603-871/Domain: protein kinase homology <KIN>

F:894-960/Domain: SAM homology <SAM>

Query Match 91.3%; Score 5088; DB 2; Length 970;  
Best Local Similarity 99.5%; Pred. No. 1.2e-231;

Matches 966; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY	15	LLAAVEELTMOSTTAETALGMMVHPSPSGMEFVSGVDENNTIRTYQVGNVPESSQNNLR	74
DB	1	LLAAVEELTMOSTTAETALGMMVHPSPSGMEFVSGVDENNTIRTYQVGNVPESSQNNLR	60
QY	75	TKFIRRGARHRIHVMKESVSDCSIPSPGCKETFNLYYYEADFDSATKTFPMWENP	134
DB	61	TKFIRRGARHRIHVMKESVSDCSIPSPGCKETFNLYYYEADFDSATKTFPMWENP	120
QY	135	WKVDTTIADESFSQVDIGRVMKINTVRSFGPSRSGFLLAFODYGGCSLLAVRFY	194
DB	121	WKVDTTIADESFSQVDIGRVMKINTVRSFGPSRSGFLLAFODYGGCSLLAVRFY	180
QY	195	RKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCGNDEMLVPIGR	254
DB	181	RKCPRIIONGAIPOETLSGAESTSLVAARGSCIANAEVDVPIKLYCGNDEMLVPIGR	240
QY	255	MCKAGFEAVENGTVCRGPGSGTFKANQDEACTHCPINSRTTBGATNCVCRNGYRADL	314
DB	241	MCKAGFEAVENGTVCRGPGSGTFKANQDEACTHCPINSRTTBGATNCVCRNGYRADL	300
QY	315	DLDMPCCTTISAPPAVIVSVNETSLMELMTPPRDSGREDLVNIIKSCSGSGGACTR	374
DB	301	DLDMPCCTTISAPPAVIVSVNETSLMELMTPPRDSGREDLVNIIKSCSGSGGACTR	360
QY	375	CGDNVQVAPROLGLTEPRITVSDLLAHQYTFEIQAVNVGTDQSPFSPQFASVNTTNOA	434
DB	361	CGDNVQVAPROLGLTEPRITVSDLLAHQYTFEIQAVNVGTDQSPFSPQFASVNTTNOA	420
QY	435	APSAVSIHQVSRVTDSTLMSQDPQNGVILDYELQYEREKESXYATAIKSTNTVT	494
DB	421	APSAVSIHQVSRVTDSTLMSQDPQNGVILDYELQYEREKESXYATAIKSTNTVT	480
QY	495	VOGLKAGAIYVQVARTVAGYGRSGMVFQMTAEYQTSIOEKLPLIGSSAGLVF	554
DB	481	--GLKAGAIYVQVARTVAGYGRSGMVFQMTAEYQTSIOEKLPLIGSSAGLVF	538
QY	555	LIAVVVIAIVCNRRGFEPADESYTDKLOHYTSGHMTPEMKTYIDPFYEDPNEAVEBP	614
DB	539	LIAVVVIAIVCNRRGFEPADESYTDKLOHYTSGHMTPEMKTYIDPFYEDPNEAVEBP	598
QY	615	EIDISCVAIEQVIGGEFVSCGHLKPKGRKEIFVAIKTLKSGYTEKORBDPSEASIM	674
DB	599	EIDISCVAIEQVIGGEFVSCGHLKPKGRKEIFVAIKTLKSGYTEKORBDPSEASIM	658
QY	675	GQFDHPNVIHLEGVVTKSTPVMIIITEFMENGLDSFLRQNDGQFTVIQVGMLEGIAAGM	734
DB	659	GQFDHPNVIHLEGVVTKSTPVMIIITEFMENGLDSFLRQNDGQFTVIQVGMLEGIAAGM	718
QY	735	KYLADNMYVHRDLAARNILVNSNLYCKVSDRGLSARFLEDPSTPYSALGKPIRPTA	794
DB	719	KYLADNMYVHRDLAARNILVNSNLYCKVSDRGLSARFLEDPSTPYSALGKPIRPTA	778
QY	795	PEAIQYRKFTSASDVWSYGIYVMEVMSYGERPYDMTQDVINAIEQDYRLPPMDCPSA	854
DB	779	PEAIQYRKFTSASDVWSYGIYVMEVMSYGERPYDMTQDVINAIEQDYRLPPMDCPSA	838
QY	855	LHQLMLDQWQDRNHRPFQGIYVNTLDMGTYNNPNSLRAMALSGSINPLLDRTTIPDTS	914
DB	839	LHQLMLDQWQDRNHRPFQGIYVNTLDMGTYNNPNSLRAMALSGSINPLLDRTTIPDTS	898
QY	915	FNTVDWELEAIKMGQYKESFANAGFTSPDVVSQMMWEDILVGTTLGQKXINSICVM	974
DB	899	FNTVDWELEAIKMGQYKESFANAGFTSPDVVSQMMWEDILVGTTLGQKXINSICVM	958
QY	975	RAQVNOIQOSVE 985	
DB	959	RAQVNOIQOSVE 969	

Search completed: August 28, 2004, 04:14:05  
Job time : 35.1156 secs





Db	138	WMENPMVKVDTTIAADSFSGVQVDLGGVWKINIEVASFQVSRNGYLAFCQYGGCNSLIA	157
Qy	190	VRVYFRKCPRIIIONGAIPOETLSGAESTSLVARASCIANAEVDVPIKLYCNDDGEMLV	249
Db	198	VRVYFRKCPRIIONGAIPOETLSGAESTSLVARASCIANAEVDVPIKLYCNDDGEMLV	257
Qy	250	PIGRCMKAGFEAVENGYTCRCGPSTFFANQGDACHCHCINRPTTSEAGTNCVNGY	309
Db	258	PIGRCMKAGFEAVENGYTCRCGPSTFFANQGDACHCHCINRPTTSEAGTNCVNGY	317
Qy	310	YRADLDELMDPCTTIPSAPOAVISVNETSLMLEWTPRDSGREDLVYNIICKSCSGR	369
Db	318	YRADLDELMDPCTTIPSAPOAVISVNETSLMLEWTPRDSGREDLVYNIICKSCSGR	377
Qy	370	GACTRCODNVQVAPROLGLTEPRYISDLHAHTQTEFLQAVNGVTQSPSPQFASVNI	429
Db	378	GACTRCODNVQVAPROLGLTEPRYISDLHAHTQTEFLQAVNGVTQSPSPQFASVNI	437
Qy	430	TTNQAAPSAVISINHQSRTVDSITLSWSQDDPNVILIDYLOYYEKELSEYNATAIKSP	489
Db	438	TTNQAAPSAVISINHQSRTVDSITLSWSQDDPNVILIDYLOYYEKELSEYNATAIKSP	497
Qy	490	TNTVTVOGLKAGAIYFQVARTVAGYGRYSKMYFOYMTAEVQTSIOETPLIICSSA	549
Db	498	TNTVTVOGLKAGAIYFQVARTVAGYGRYSKMYFOYMTAEVQTSIOETPLIIVGSSA	557
Qy	550	AGLVPLIAVVVAIAVGNRRGPERABSEYTDKLOHTSGMTPGKIIYIDPTEYEDPNEAV	609
Db	558	AGLVPLIAVVVAIAVGNRRGPERABSEYTDKLOHTSGMTPGKIIYIDPTEYEDPNEAV	617
Qy	610	REBAKHEIDISCVKIEQVITAGSPGVCSGHLKPEKREIFAITKLSGTEKORRPLFS	669
Db	618	REBAKHEIDISCVKIEQVITAGSPGVCSGHLKPEKREIFAITKLSGTEKORRPLFS	677
Qy	670	EASIMGQFHPNVIHLEGVIVTSFTVMIITFERMNGSLDSFLRQNDQFTVIQVYGLKRG	729
Db	678	EASIMGQFHPNVIHLEGVIVTSFTVMIITFERMNGSLDSFLRQNDQFTVIQVYGLKRG	737
Qy	730	IAAGMYLADMYNHHDLAARNILVNSULVCVSPFGSLRELEDTSDDPYTALGCKIP	789
Db	738	IAAGMYLADMYNHHDLAARNILVNSULVCVSPFGSLRELEDTSDDPYTALGCKIP	797
Qy	790	IRMTAEALIQYKFTSASDVMYSYGIWMEVMSYGERPYMDTNDVINALIEODYRLPPM	849
Db	798	IRMTAEALIQYKFTSASDVMYSYGIWMEVMSYGERPYMDTNDVINALIEODYRLPPM	857
Qy	850	DGCSALHQLMDQWQDRNHRPRKFOIYNLTDKXIRNNSLKAAAPLSSGJNPLDRTI	909
Db	858	DGCSALHQLMDQWQDRNHRPRKFOIYNLTDKXIRNNSLKAAAPLSSGJNPLDRTI	917
Qy	910	PDYTSFNTYDEMLEALIKMGQYKESFANAGFTSFVVSQMMEDILRAGVTLAGHOKKILN	969
Db	918	PDYTSFNTYDEMLEALIKMGQYKESFANAGFTSFVVSQMMEDILRAGVTLAGHOKKILN	977
Qy	970	SIQWRAQNNQIOSVE	985
Db	978	SIQWRAQNNQIOSVE	993

Search completed: August 28, 2004, 04:12:52  
Job time : 103.898 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 03:50:04 ; Search time 104.415 Seconds  
(without alignments)  
2854.849 Million cell updates/sec

Title: US-09-914-883-4  
Sequence: 1 MALRRLGALLLLPLLAAYE.....QGIFPKDSKHSNDSCGG 1055

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Genesegp29Jan04:\*  
2: genesegp1980s:\*  
3: genesegp1990s:\*  
4: genesegp2000s:\*  
5: genesegp2001s:\*  
6: genesegp2002s:\*  
7: genesegp2003as:\*  
8: genesegp2003bs:\*  
9: genesegp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5571	100.0	1055	3 AAB19591	Human CAS
2	5571	100.0	1055	6 AB007847	Human eph
3	5170.5	92.8	987	3 AAB19590	Human CAS
4	5129	92.1	994	2 AAW26366	Mouse Nuk
5	5129	92.1	994	4 AAU01907	Murine ne
6	5125	92.0	984	2 AAR87018	Receptor
7	5092	91.4	970	2 AAR85089	EPH-like

ALIGNMENTS

RESULT 1  
ID AAB19591 standard; protein; 1055 AA.

XX AAB19591;

DT 22-JAN-2001 (first entry)

DE Human CASB616.

KW CASB616; EPHB2; ERK; EPH3; EPHT3; DRT; HEK5; EPHB2V;

KM receptor protein tyrosine kinase; human; antigen; colon cancer; ovary cancer; autoimmune disease; vaccine; therapy; diagnosis.

XX Homo sapiens.  
OS WO2000053216-A2.  
XX 14-SEP-2000.  
XX 28-FEB-2000; 2000MO-EP001587.  
XX 05-MAR-1999; 99GB-00005124.  
XX (SMIK ) SWITKLINE BEECHAM BIOLOGICALS.  
XX Vinals Y De Bassols.  
XX WPI; 2000-587384/55.  
XX N-PSDB; AAA88549.  
XX Vaccine composition for treating ovarian and colon cancer, comprises  
PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
PT expressing the polypeptides.  
XX Claim 1; Page 42; 57pp; English.  
XX The present sequence is that of human CASB616, a member of the EPH and  
CC EPH-related family of receptor protein tyrosine kinases. CASB616 is also  
CC known as EPHB2, ERK, EPH3, EPHT3, DRT, HEK5 and EPHB2V. CASB616  
CC polypeptides and polynucleotides are important immunogens for specific  
CC prophylactic or therapeutic immunization against tumours, especially  
CC colon cancer (claimed) and ovarian cancer. They are specifically  
CC expressed or highly over-expressed in tumours compared to normal cells  
CC and can thus be targeted by antigen-specific immune mechanisms leading to  
CC destruction of the tumour cells. They can also be used to diagnose the  
CC occurrence of tumour cells. Their inappropriate expression can also cause  
CC an induction of autoimmune responses, which can be corrected through  
CC vaccination using the CASB616 polypeptides or polynucleotides  
XX Sequence 1055 AA;

Query Match 100.0%; Score 5571; DB 3; Length 1055;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALRRLGALLLLPLLAAYEETLMDSTTAALGMAVHPSPGMEVSGVDENNTIRTYQ 60  
DB 1 MALRRLGALLLLPLLAAYEETLMDSTTAALGMAVHPSPGMEVSGVDENNTIRTYQ 60  
QY 1 VCNVFESSQNNWMLRKFRRRGARHIVEMKFSVRDCSSIPSVGSCKETENLYYEADF 120  
DB 1 VCNVFESSQNNWMLRKFRRRGARHIVEMKFSVRDCSSIPSVGSCKETENLYYEADF 120  
QY 121 DSATKTFEPMNEMENPVKVDITAADESFSQVDLGKRVKINTEVRSFGVSSGTYLAFOQ 180  
DB 121 DSATKTFEPMNEMENPVKVDITAADESFSQVDLGKRVKINTEVRSFGVSSGTYLAFOQ 180  
QY 121 DSATKTFEPMNEMENPVKVDITAADESFSQVDLGKRVKINTEVRSFGVSSGTYLAFOQ 180  
DB 121 DSATKTFEPMNEMENPVKVDITAADESFSQVDLGKRVKINTEVRSFGVSSGTYLAFOQ 180  
QY 181 YGGCMSLIAVAVFRRKCRITLQNGAIFQETLSGAEFSISLVAAKSGCTANAEVVPITLY 240  
DB 181 YGGCMSLIAVAVFRRKCRITLQNGAIFQETLSGAEFSISLVAAKSGCTANAEVVPITLY 240  
QY 241 CNGDEWLVPIGRGCKGKFAVENGTVCRCGPGTFKANGDAGACTHCPINSRTTSGA 300  
DB 241 CNGDEWLVPIGRGCKGKFAVENGTVCRCGPGTFKANGDAGACTHCPINSRTTSGA 300  
QY 301 TNCVCRNGCYRADLDPLDMCTTTPSAPQAVISSVNETSLMLWTPPRDSGGRDLYNI 360  
DB 301 TNCVCRNGCYRADLDPLDMCTTTPSAPQAVISSVNETSLMLWTPPRDSGGRDLYNI 360  
QY 361 ICKSCSGRGACTCGDGVQYAPROLGLTEPRYISDLATQYTFELQANGVTDQSPF 420  
DB 361 ICKSCSGRGACTCGDGVQYAPROLGLTEPRYISDLATQYTFELQANGVTDQSPF 420  
QY 421 SPQFASVNTTNGAAPSASVIMHGVSRVDSITLSWSQPDQPNGVILDELYQYEKELSE 480  
DB 421 SPQFASVNTTNGAAPSASVIMHGVSRVDSITLSWSQPDQPNGVILDELYQYEKELSE 480

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Db 421 SPOFASVNTTNOAPSAVSIHQVSRITDSTLSNSQDPQNGVILIDYELQYKEKLE 480
QY 481 YNATAIKSPNTNTVQGLKAGAIYVQVBARVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
Db 481 YNATAIKSPNTNTVQGLKAGAIYVQVBARVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
QY 541 LPLITSSAGVFLIAVNVVIAIVCNRRGFEADSEYTDLQHYTSGHMTGPKKIYIDPF 600
Db 541 LPLITSSAGVFLIAVNVVIAIVCNRRGFEADSEYTDLQHYTSGHMTGPKKIYIDPF 600
QY 601 TYEDPNAVEFAKEIDISCVKIEQVIGAGEFGEVSGHKLPGKKEIFVAIKTLKSGYT 660
Db 601 TYEDPNAVEFAKEIDISCVKIEQVIGAGEFGEVSGHKLPGKKEIFVAIKTLKSGYT 660
QY 661 EKQRRDLSASIMGQDHPNVILHSGVTKSTPWNIIIEFPMNSLDSFLRNDQGFY 720
Db 661 EKQRRDLSASIMGQDHPNVILHSGVTKSTPWNIIIEFPMNSLDSFLRNDQGFY 720
QY 721 IQLVGMKRGIAAGKYLADNMYHRLAARNILVNSNLCKVSDFGLSRFLSDTSDPY 780
Db 721 IQLVGMKRGIAAGKYLADNMYHRLAARNILVNSNLCKVSDFGLSRFLSDTSDPY 780
QY 781 TSAIGKIPRTWAPPAIQRKTTASDVWSYGIIVMEVMSYGERPYMDMTVDVINAIE 840
Db 781 TSAIGKIPRTWAPPAIQRKTTASDVWSYGIIVMEVMSYGERPYMDMTVDVINAIE 840
QY 841 QDRLPPMDCPSALHQLMDCKQKRNHRPKFGQVNTLDKIRRNPSLXMAPSSGI 900
Db 841 QDRLPPMDCPSALHQLMDCKQKRNHRPKFGQVNTLDKIRRNPSLXMAPSSGI 900
QY 901 NLPLDRTIDYTSFNTVDEMLAIKMGQYKESFANAGFTSPDVASQMMEDILRAGVTL 960
Db 901 NLPLDRTIDYTSFNTVDEMLAIKMGQYKESFANAGFTSPDVASQMMEDILRAGVTL 960
QY 961 AGHOKTILNSIQVRAQMNQIQSVEGQPLARRPRAQRTKRCOPRYTKTCSNDSGKK 1020
Db 961 AGHOKTILNSIQVRAQMNQIQSVEGQPLARRPRAQRTKRCOPRYTKTCSNDSGKK 1020
QY 1021 GMGKKTDPGRGREIQGIFPKDSHESNDCSCG 1055
Db 1021 GMGKKTDPGRGREIQGIFPKDSHESNDCSCG 1055

RESULT 2
ABU07847 standard; protein; 1055 AA.
ID ABU07847
AC ABU07847;
XX
DT 10-MAY-2003 (first entry)
XX
DE Human ephrin receptor ligand EphB2.
XX
KW Cytostatic; vasodilator; antiinflammatory; cardiact; gene therapy;
KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW cell migration disorder; cell proliferation disorder; neovascularisation;
KW ischaemia; infarction; tissue graft; transplant; human;
KW ephrin receptor ligand; tie receptor tyrosine kinase; EphB2.
XX
OS Homo sapiens.
XX
PN MO2003004523-AA2.
XX
PD 16-JAN-2003.
XX
PF 02-JUL-2002; 2002WO-IB002524.
XX
PR 02-JUL-2001; 2001US-0302960P.
XX
PA (LICN ) LICENTIA LTD.
XX
PI Aitalo K, Kubo H;

```

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XX WP1: 2003-210341/20.
DR N-PSDB; ABX12548.
XX
PT Identifying modulators of binding between a Tie receptor tyrosine kinase
PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.
PS Disclosure; Page 128-132; 199pp; English.
XX
CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or new or
CC neovascularization (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human EphB2, a member of the Ephrin-B subfamily of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Ephrin receptor ligands
SQ Sequence 1055 AA:
Query Match 100.0%; Score 5571; DB 6; Length 1055;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1055; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALRRLGAILLLPLAAVEETLMDSTTATAEIGMWHYPPSGWEVSGYDENNTIRTYQ 60
Db 1 MALRRLGAILLLPLAAVEETLMDSTTATAEIGMWHYPPSGWEVSGYDENNTIRTYQ 60
QY 61 VCNVFESSQNNWLTKEIRRRGARHIVEMKFSVRDSSIPSYPGSKETFNLYYEADF 120
Db 61 VCNVFESSQNNWLTKEIRRRGARHIVEMKFSVRDSSIPSYPGSKETFNLYYEADF 120
QY 121 DSATKTFPNNMENWVVDITIADESFSQVDLGRVWKITNTERSGPVRSRGFYAFQD 180
Db 121 DSATKTFPNNMENWVVDITIADESFSQVDLGRVWKITNTERSGPVRSRGFYAFQD 180
QY 121 DSATKTFPNNMENWVVDITIADESFSQVDLGRVWKITNTERSGPVRSRGFYAFQD 180
Db 121 DSATKTFPNNMENWVVDITIADESFSQVDLGRVWKITNTERSGPVRSRGFYAFQD 180
QY 181 YGCGMSLIAVVFYRKCPRIIQNGAIFQETLSGAEESTLVAARGSCIANAEEDVPILKY 240
Db 181 YGCGMSLIAVVFYRKCPRIIQNGAIFQETLSGAEESTLVAARGSCIANAEEDVPILKY 240
QY 241 CNGDEWLVPIGRMCGAGFEAVENGTVCGSGRTFKANOGDPACTHCHINRSTSEGA 300
Db 241 CNGDEWLVPIGRMCGAGFEAVENGTVCGSGRTFKANOGDPACTHCHINRSTSEGA 300
QY 301 TNCVCRAGYRADLDPDMCTTIPSAPOAVISVNTSMLMTWPPRDSGREDLVYNI 360
Db 301 TNCVCRAGYRADLDPDMCTTIPSAPOAVISVNTSMLMTWPPRDSGREDLVYNI 360
QY 361 ICXSGSGRGACTREGNVOYAPROGLTEPRRIYISDLAHTOYTFEIQAVNGVTDOSP 420
Db 361 ICXSGSGRGACTREGNVOYAPROGLTEPRRIYISDLAHTOYTFEIQAVNGVTDOSP 420
QY 421 SPOFASVNTTNOAPSAVSIHQVSRITDSTLSNSQDPQNGVILIDYELQYKEKLE 480
Db 421 SPOFASVNTTNOAPSAVSIHQVSRITDSTLSNSQDPQNGVILIDYELQYKEKLE 480
QY 481 YNATAIKSPNTNTVQGLKAGAIYVQVBARVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
Db 481 YNATAIKSPNTNTVQGLKAGAIYVQVBARVAGYGRYSGKXYFQMTAEAYQTSIOEK 540
QY 541 LPLITSSAGVFLIAVNVVIAIVCNRRGFEADSEYTDLQHYTSGHMTGPKKIYIDPF 600

```

DB 541 LPLIGSSAAGLVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTGPKKIYIDPF 600  
XX  
QY 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVALIKTKSGYT 660  
DB 601 TYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVALIKTKSGYT 660  
QY 661 EXKORDFLSEASIMGQFDHPNVILHEGVYTKSPVMIITEFMENGLSDSFLRQNDQOFTV 720  
DB 661 EXKORDFLSEASIMGQFDHPNVILHEGVYTKSPVMIITEFMENGLSDSFLRQNDQOFTV 720  
QY 721 IGVVGLRGIAGCKYLAQNMVYHRLAARNTLVNSLVCKISDFLSFLLEDSDPTV 780  
DB 721 IGVVGLRGIAGCKYLAQNMVYHRLAARNTLVNSLVCKISDFLSFLLEDSDPTV 780  
QY 781 TSLGKRIPIRMTAPPAIQYRKFTSADVWSYGVVWKEVMSYGERPYMTNTQDYVNAIE 840  
DB 781 TSLGKRIPIRMTAPPAIQYRKFTSADVWSYGVVWKEVMSYGERPYMTNTQDYVNAIE 840  
QY 841 QDYRLPPEMDCPGSAHQMLDMCQKDRNRPKFGQIVNTLDMKIRPNLSLKAMAPLISGI 900  
DB 841 QDYRLPPEMDCPGSAHQMLDMCQKDRNRPKFGQIVNTLDMKIRPNLSLKAMAPLISGI 900  
QY 901 NPLDLRTPIDYTSFNTVDMLBAIKMGQYKESFANAGFTSPDVYSOMMMEDILKVGVTL 960  
DB 901 NPLDLRTPIDYTSFNTVDMLBAIKMGQYKESFANAGFTSPDVYSOMMMEDILKVGVTL 960  
QY 961 AGHQKILNLSIQVRAQNMQIQSVESQPLARPRATGTRKCPQPDVTKTKCNSNDGKKX 1020  
DB 961 AGHQKILNLSIQVRAQNMQIQSVESQPLARPRATGTRKCPQPDVTKTKCNSNDGKKX 1020  
QY 1021 GMGKKTIDPRGRREIQIFPKEDSHKESNDSCSG 1055  
DB 1021 GMGKKTIDPRGRREIQIFPKEDSHKESNDSCSG 1055

RESULT 3  
AAB19590  
ID AAB19590 standard; protein: 987 AA.  
XX  
AC AAB19590;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE Human CASB616.  
XX  
KW CASB616; EPHB2; ERK; EPH3; EPH3; DRT; HEK5; EPHB2v;  
KW receptor protein tyrosine kinase; human; antigen; colon cancer;  
XX ovary cancer; tumour; autoimmune disease; vaccine; therapy; diagnosis.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 568..569  
FT /note="an additional Arg residue decodes from the  
FT CASB616 nucleotide sequence given in the specification  
FT (see AAB8548), but is not given in the CASB616 amino  
FT acid sequence in the specification"  
FT Misc-difference 956  
FT /note="encoded by GTT"  
XX  
FT  
XX  
PN W0200053216-A2.  
XX  
PD 14-SEP-2000.  
XX  
PE 28-FEB-2000; 2000MO-EP001587.  
XX  
PR 05-MAR-1999; 99GB-00005124.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Vinala Y De Basolac;  
XX  
DR WPI; 2000-587384/55.

DR N-PSDB; AAA8548.  
XX  
XX Vaccine composition for treating ovarian and colon cancer, comprises  
PT CASB616 polypeptides, polynucleotides or antigen presenting cells  
PT expressing the polypeptides.  
XX  
XX Claim 1; Page 41; 57pp; English.  
XX  
CC The present sequence is that of human CASB616, a member of the Eph  
CC Eph-related family of receptor protein tyrosine kinases. CASB616 is also  
CC known as EPHB2, ERK, EPH3, EPH3, DRT, HEK5 and EPHB2v. CASB616  
CC polypeptides and polynucleotides are important immunogens for specific  
CC prophylactic or therapeutic immunization against tumours, especially  
CC colon cancer (claimed) and ovarian cancer. They are specifically  
CC expressed or highly over-expressed in tumours compared to normal cells  
CC and can thus be targeted by antigen-specific immune mechanisms leading to  
CC destruction of the tumour cells. They can also be used to diagnose the  
CC occurrence of tumour cells. Their inappropriate expression can also cause  
CC an induction of autoimmune responses, which can be corrected through  
CC vaccination using the CASB616 polypeptides or polynucleotides  
XX  
SQ Sequence 987 AA;  
Query Match 92.8%; Score 5170.5; DB 3; Length 987;  
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;  
Matches 984; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MALRLGALLLLPLLAVEETLMDSTTAELGMYVHPESGWEVSGYDENNTIRTYQ 60  
DB 1 MALRLGALLLLPLLAVEETLMDSTTAELGMYVHPESGWEVSGYDENNTIRTYQ 60  
QY 61 VCNVPESSQNNWLTKPIRRGARRIHVEMKFSVRDSSISVSGCKETNLXYEADF 120  
DB 61 VCNVPESSQNNWLTKPIRRGARRIHVEMKFSVRDSSISVSGCKETNLXYEADF 120  
QY 121 DSATKTFPMNMENPMVKVDITNADESFSQVLDLGRVWVKINTEVASFVSRSGFYLAFO 180  
DB 121 DSATKTFPMNMENPMVKVDITNADESFSQVLDLGRVWVKINTEVASFVSRSGFYLAFO 180  
QY 181 YGGCWSLIAVVFPRKCPRIITONGALFOETLSGAEISLVAAKSCIANAEVDPVPLXY 240  
DB 181 YGGCWSLIAVVFPRKCPRIITONGALFOETLSGAEISLVAAKSCIANAEVDPVPLXY 240  
QY 241 CNGDGEWLVPIGRCKXGFEAVENGATVRCGPGSTFKANAGDACHPCIPNSRTSSGA 300  
DB 241 CNGDGEWLVPIGRCKXGFEAVENGATVRCGPGSTFKANAGDACHPCIPNSRTSSGA 300  
QY 301 TNCVCRNGYRADLDPDLPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGRDLYVNI 360  
DB 301 TNCVCRNGYRADLDPDLPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGRDLYVNI 360  
QY 361 ICKSGSGRGACTCGDNVQYAPROLGLTEPRITYSDLAATQVTFELQANGVYDQSPF 420  
DB 361 ICKSGSGRGACTCGDNVQYAPROLGLTEPRITYSDLAATQVTFELQANGVYDQSPF 420  
QY 421 SPOFASVITITNOAPASVSIIMHQVSRVDSITLSWSQPDQPNVILDEYELQYKELSE 480  
DB 421 SPOFASVITITNOAPASVSIIMHQVSRVDSITLSWSQPDQPNVILDEYELQYKELSE 480  
QY 481 YNATAIKSPNTVTVYOGI-KAGAIYVFOVRARTVAGYGSYSGKMPQMTTEAYQTSIOEK 540  
DB 481 YNATAIKSPNTVTVYOGI-KAGAIYVFOVRARTVAGYGSYSGKMPQMTTEAYQTSIOEK 540  
QY 541 LPLIGSSAAGLVFLIAVVVIAIVCN-RGFERADSEYTDKLOHYTSGHMTGPKKIYIDP 599  
DB 541 LPLIGSSAAGLVFLIAVVVIAIVCNRRRGFERADSEYTDKLOHYTSGHMTGPKKIYIDP 600  
QY 600 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVALIKTKSGY 659  
DB 601 FTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVALIKTKSGY 660  
QY 660 TEKORDFLSEASIMGQFDHPNVILHEGVYTKSPVMIITEFMENGLSDSFLRQNDQOFT 719

Db 661 TEKGRDPLSBSASIMGQFDHPNVIHLGVTTKSTPVMIIIEFMENGLSDSFLRQNDQOFT 720  
 QY 720 VIQVGMRLRGIAAGMKYLAQNNVYVRDLAARNTLVNSNLVCYKSDGLSFLEDDTSDPT 779  
 Db 721 VIQVGMRLRGIAAGMKYLAQNNVYVRDLAARNTLVNSNLVCYKSDGLSFLEDDTSDPT 780  
 QY 780 YTSALGSKTIPRTWAPALQYRKFTSASDVSYGYIMWEVMSYGERPYMDNTNOVINAI 839  
 Db 781 YTSALGSKTIPRTWAPALQYRKFTSASDVSYGYIMWEVMSYGERPYMDNTNOVINAI 840  
 QY 840 EODRPLPPMDCPSEALHQLMLDCQKDRNRHPRFGQIVNTLDKIRNPNSIKAMAPLSSG 899  
 Db 841 EODRPLPPMDCPSEALHQLMLDCQKDRNRHPRFGQIVNTLDKIRNPNSIKAMAPLSSG 900  
 QY 900 INPPLDRTIPDYTSFNTVDEMLDAIKMGQYKESFANAGFTSPDVVSQMMEDILRVGT 959  
 Db 901 INPPLDRTIPDYTSFNTVDEMLDAIKMGQYKESFANAGFTSPDVVSQMMEDILRVGT 960  
 QY 960 LAGHOKKILNSIQVMPRAQNNQIOSVE 985  
 Db 961 LAGHOKKILNSIQVMPRAQNNQIOSVE 986

RESULT 4  
 ID AAW26366  
 AAW26366 standard; protein; 994 AA.  
 AC AAW26366;  
 DT 02-DEC-1997 (first entry)  
 XX  
 DE Mouse Nuk tyrosine kinase.  
 KW Nuk tyrosine kinase; Eph receptor tyrosine kinase; signal transduction;  
 KW acronogenesis; neurodegenerative disease; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; multiple sclerosis;  
 KW amyotrophic lateral sclerosis; Wernicke's disease; nerve damage; trauma;  
 KW ischaemia; stroke.  
 XX  
 OS Mus musculus.  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= Sig\_peptide  
 FT Protein 27..994  
 FT /label= Mat\_protein  
 FT Domain 27..548  
 FT /label= Extracellular\_domain  
 FT Region 330..420  
 FT /label= FNIII  
 FT Region /note= "Fibronectin type III repeat"  
 FT /label= FNIII  
 FT /note= "Fibronectin type III repeat"  
 FT Domain 548..574  
 FT /label= Transmembrane\_domain  
 FT Domain 575..994  
 FT /label= Cytoplasmic\_domain  
 FT Region 623..888  
 FT /label= Tyrosine-kinase\_region  
 PN MO9714966-A1.  
 PD 24-APR-1997.  
 XX  
 PF 10-OCT-1996; 96WO-CA000679.  
 XX  
 PR 13-OCT-1995; 95US-0005518P.  
 PA (MOUNT) MOUNT SINAI HOSPITAL CORP.  
 PI Pawson A, Henkemeyer M;  
 XX

DR WPI, 1997-245245/22.  
 DR N-PSDB; AAT84528.  
 PT Activation of ligand regulatory pathways by Eph subfamily receptor  
 PT tyrosine kinases - for stimulating or inhibiting axonogenesis, useful for  
 PT treatment of e.g. neurodegenerative diseases such as Alzheimer's or  
 PT Parkinson's diseases.  
 PS Disclosure; Fig 3; 55pp; English.  
 XX  
 CC Murine Nuk tyrosine kinase is an Eph subfamily receptor tyrosine kinase  
 CC that is essential for formation of the medial tract of the anterior  
 CC commissure of the brain, and which appears to play a role in the  
 CC formation of the habenular interpeduncle tract. Its amino acid sequence  
 CC was deduced from cDNA clones (see AAT84528) isolated from an embryo cDNA  
 CC library. The extracellular domain of Nuk was shown to be sufficient for  
 CC formation of the medial tract. Eph subfamily receptor tyrosine kinases  
 CC (e.g. the Nuk extracellular domain) can be used in claimed methods to:  
 CC activate a ligand regulatory pathway in a cell; identify substances able  
 CC to bind a ligand for an Eph subfamily receptor tyrosine kinase; and to  
 CC affect neuronal development or regeneration, especially the stimulation  
 CC or inhibition of axonogenesis, in a mammal. Activation of the ligand  
 CC regulatory pathway results in downstream activation of a series of  
 CC cytoskeletal architecture, cell metabolism, cell migration and cell-cell  
 CC interactions. Substances which activate the ligand regulatory pathway may  
 CC be used for stimulating or inhibiting neuronal development regeneration  
 CC and axonal migration associated with neurodegenerative disease e.g.  
 CC Alzheimer's, Parkinson's or Huntington's diseases, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, deficiency diseases such as Wernicke's  
 CC disease, peripheral nerve damage, trauma and ischaemia resulting from  
 CC stroke  
 CC  
 SQ Sequence 994 AA:  
 Query Match 92.1%; Score 5129; DB 2; Length 994;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 LLLPLLAAYEETIMDSITTAETLGGMMVHPSPGMEVSYGDENNTITRTQVGNVPESSQ 69  
 Db 18 LLLPLLAAYEETIMDSITTAETLGGMMVHPSPGMEVSYGDENNTITRTQVGNVPESSQ 77  
 QY 70 NNWLRTKFIIRRGARHRIHVEKESVPRDCSSIPSPGSKETFNLYYEADFDSATKTFPN 129  
 Db 78 NNWLRTKFIIRRGARHRIHVEKESVPRDCSSIPSPGSKETFNLYYEADFDSATKTFPN 137  
 QY 130 WMENPMYKVDITIADEFSQVDJGGRYMKINTVRSRGPYSRGGFYAFADYGGCWSLIA 189  
 Db 138 WMENPMYKVDITIADEFSQVDJGGRYMKINTVRSRGPYSRGGFYAFADYGGCWSLIA 197  
 QY 190 VRVFRKCPRIQNGALFOETLSGAESTSLVAARGSCINAAEEDVPIKLYCNGDGEMLV 249  
 Db 198 VRVFRKCPRIQNGALFOETLSGAESTSLVAARGSCINAAEEDVPIKLYCNGDGEMLV 257  
 QY 250 FIGRCYKAGBEAVENGTVRGCPBSGTFKANKOGDEACTHCPINSKRTTSEATNVCVCRNGY 309  
 Db 258 FIGRCYKAGBEAVENGTVRGCPBSGTFKANKOGDEACTHCPINSKRTTSEATNVCVCRNGY 317  
 QY 310 YRADLDPLMDPCTTIPAPQAVTSVNETSLMEFTPPRDSGREDLVNIIKSCGSGSR 369  
 Db 318 YRADLDPLMDPCTTIPAPQAVTSVNETSLMEFTPPRDSGREDLVNIIKSCGSGSR 377  
 QY 370 GACTRCGDNVQYARQGLTEPRYISDLIAHTQYFEIQAQVNGVTIDQSPFSQFASVNI 429  
 Db 378 GACTRCGDNVQYARQGLTEPRYISDLIAHTQYFEIQAQVNGVTIDQSPFSQFASVNI 437  
 QY 430 TTNGAAPSASIMHOVRATVDSITLISGSDPDQNGVILDOELOYEKEISEVNAATIKSP 489  
 Db 438 TTNGAAPSASIMHOVRATVDSITLISGSDPDQNGVILDOELOYEKEISEVNAATIKSP 497  
 QY 490 TTTVTVOGLKAGAIYVQVARTVAGYGRYSGMYEQMTAEAYQTSIOEKPLIIIGSSA 549

Db 498 TMTVTGGLKAGAIYFQVAPARTVAGYGRYSGMVFQMTAEVQTSIEKPLIVGSSA 557  
QY 550 AGIVFLAAVVVIAIVCNRRGFERADSEYTDKLOHTYSGHNTPMKRIYIDPFYEDPNEAY 609  
Db 558 AGIVFLAAVVVIAIVCNRRGFERADSEYTDKLOHTYSGHNTPMKRIYIDPFYEDPNEAY 617  
QY 610 REPAKSIDSCVKIEVYIGAGFGEVCSGHLKPGKREIFVAIKITLKSQYTERKORDPFS 669  
Db 618 REPAKSIDSCVKIEVYIGAGFGEVCSGHLKPGKREIFVAIKITLKSQYTERKORDPFS 677  
QY 670 EASIMQGFPHNVTHIEGVVTKSTPWIIEPEMENSLSLSPRONQGFVIVQLVGMMLG 729  
Db 678 EASIMQGFPHNVTHIEGVVTKSTPWIIEPEMENSLSLSPRONQGFVIVQLVGMMLG 737  
QY 730 IAAGMKYLDAMNYVHDLAARNILVNSNLVCVSDGSLRFLDDTSDPTYSALGKIP 789  
Db 738 IAAGMKYLDAMNYVHDLAARNILVNSNLVCVSDGSLRFLDDTSDPTYSALGKIP 797  
QY 790 IRTTAEALIOYKFTASDVWYSGIWMYEMVSGEPPYMDMTQDVINALIEDQYRLPPM 849  
Db 798 IRTTAEALIOYKFTASDVWYSGIWMYEMVSGEPPYMDMTQDVINALIEDQYRLPPM 857  
QY 850 DCPSSALHQLMLDCMQKDRNRPFGQIVNTLDMINPNLSLKAMAPLSSGINLPILDRIT 909  
Db 858 DCPSSALHQLMLDCMQKDRNRPFGQIVNTLDMINPNLSLKAMAPLSSGINLPILDRIT 917  
QY 910 PNYTSSENTVDMEIATMGQYKESFANAGFTSPVVSQMMEDILRVYVTLAGHQKKILN 969  
Db 918 PNYTSSENTVDMEIATMGQYKESFANAGFTSPVVSQMMEDILRVYVTLAGHQKKILN 977  
QY 970 SIQVRAQNMVQIOSVE 985  
Db 978 SIQVRAQNMVQIOSVE 993

RESULT 5  
AAU01907  
ID AAU01907 standard; protein; 994 AA.  
XX  
AC AAU01907;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Murine neural kinase (Nuk) polypeptide.  
XX  
KW Neural kinase; Nuk; receptor tyrosine kinase; axonal migration; stroke;  
KW nerve fibre; cell-cell interaction; axonogenesis; neuronal development;  
KW regeneration; neurodegenerative disorder; Alzheimer's disease; ischemia;  
KW Parkinson's disease; Huntington's disease; demyelinating disease;  
KW multiple sclerosis; amyotrophic lateral sclerosis; deficiency disease;  
KW Merinck's disease; nutritional polyneuropathy; multistem degeneration;  
KW progressive supranuclear palsy; Shy Drager's syndrome; mouse;  
KW olivoponto cerebellar atrophy; peripheral nerve damage.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..26 /note="Signal peptide"  
FT Domain 26..548  
FT Protein /notes="Extracellular domain, preferably residues 26-548"  
FT 27..994  
FT /note="Mature murine neural kinase"  
FT Domain 52..119  
FT /note="Ig-like domain"  
FT Region 239..268  
FT /note="Ig-like Nuk repeat"  
FT Region 330..420  
FT /note="Fibronectin type III repeat"  
FT Region 444..534  
FT /note="Fibronectin type III repeat"  
FT Domain 549..574  
FT /note="Hydrophobic transmembrane domain"

FT Binding-site 600..618  
FT /note="SH2 domain binding site"  
FT Region 601..994  
FT /note="Carboxy terminal"  
FT Modified-site 604..613  
FT /note="Phosphorylation site"  
FT Domain 623..888  
FT /note="Catalytic tyrosine kinase domain"  
FT Binding-site 623..707  
FT /note="ATP binding site"  
PN US6218356-B1.  
XX 17-APR-2001.  
PD 13-OCT-1995; 95US-00542635.  
PF 29-APR-1994; 94US-00235407.  
PR 28-APR-1995; 95MO-CA000254.  
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.  
XX Pawsen A, Henkemeyer M, Letwin K;  
PI WPI: 2001-289845/30.  
XX N-PSDB; AAS03812.  
DR New composition comprising neural receptor tyrosine kinase protein useful  
PT for inhibiting or stimulating axonogenesis, neuronal development, or  
PT regeneration and axonal migration.  
XX Claim 1; Fig 2; 86pp; English.  
PS The sequence represents a mouse neural kinase (Nuk) polypeptide. The  
XX murine Nuk locus has been mapped to the distal end of chromosome four.  
CC The polypeptide is a novel receptor tyrosine kinase protein, and is found  
CC to be expressed at high levels within migrating axons and is associated  
CC with nerve fibres. It functions to regulate specific cell-cell  
CC interactions during early development of the nervous system and in  
CC axonogenesis. Substances which bind to the Nuk protein, particularly  
CC ligands, may be used for stimulating or inhibiting neuronal development,  
CC regeneration and axonal migration associated with neurodegenerative  
CC disorders and conditions involving trauma and injury to the nervous  
CC system. These disorders include Alzheimer's disease, Parkinson's disease,  
CC Huntington's disease, demyelinating diseases such as Merinck's  
CC amyotrophic lateral sclerosis, deficiency diseases such as Merinck's  
CC disease and nutritional polyneuropathy, progressive supranuclear palsy,  
CC Shy Drager's syndrome, multistem degeneration, olivoponto cerebellar  
CC atrophy, peripheral nerve damage, and ischemia resulting from stroke.  
CC The proteins may be used to prepare antibodies having specificity for Nuk  
CC proteins, which can be used to diagnose or treat disorders of the nervous  
CC system. These proteins are also used for screening agonists or  
CC antagonists of the interactions of the Nuk proteins with binding  
CC molecules  
XX  
SQ Sequence 994 AA;  
XX  
XX  
Query Match 92.1%; Score 5129; DB 4; Length 994;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 10 LLLPLLAABEETLMDSTTATAEAGMYHPPSGMEVSGYENMTTITTYQCVVFESSQ 69  
Db 18 LLLPLLAABEETLMDSTTATAEAGMYHPPSGMEVSGYENMTTITTYQCVVFESSQ 77  
QY 70 NNMLRTKXIRRRGARIRHVEKKFSVRDCSSIPSPVSGSKETFNLYYYEADPSATKTPPN 129  
Db 78 NNMLRTKXIRRRGARIRHVEKKFSVRDCSSIPSPVSGSKETFNLYYYEADPSATKTPPN 137  
QY 130 WMENPVAKYDTTIADESSQVDLGRVWKINTEVRSFSPVRSRGFTYLAFOYGGGMSILA 189  
Db 138 WMENPVAKYDTTIADESSQVDLGRVWKINTEVRSFSPVRSRGFTYLAFOYGGGMSILA 197

QY	19	VRFVYRCPPIIONGAIPOETLSGAESTLVAAFGSCFANNAEVDVPLKLYCNDGEMLV	249
Db	198	VRFVYRCPPIIONGAIPOETLSGAESTLVAAFGSCFANNAEVDVPLKLYCNDGEMLV	257
QY	250	PIGRCKAGFEAVENGTVCRGPGSGTFKANGGDEACTHCPINSRTTSEGANVCVCHNGY	309
Db	258	PIGRCKAGFEAVENGTVCRGPGSGTFKANGGDEACTHCPINSRTTSEGANVCVCHNGY	317
QY	310	YRDLDPDLMPCCTTISAPQAVISSVNETSLMLETPRDSGGREDLVYNIICSGSGR	365
Db	318	YRDLDPDLMPCCTTISAPQAVISSVNETSLMLETPRDSGGREDLVYNIICSGSGR	377
QY	370	GACTRCGDNVQYAPRLGLTEPRYISDLTAHTQYTFEIQAVNGVTDQSPSPQFASVNI	429
Db	378	GACTRCGDNVQYAPRLGLTEPRYISDLTAHTQYTFEIQAVNGVTDQSPSPQFASVNI	437
QY	430	TTNQAAPSAVSIHMQVSRVDSITLSMSPODPNGVILIYELQYKEKELSTYNTAKSP	489
Db	438	TTNQAAPSAVSIHMQVSRVDSITLSMSPODPNGVILIYELQYKEKELSTYNTAKSP	497
QY	490	TNTVTVQGLGAGAIYVQYRARTVAGYGRSGSKMFQMTAEVQTSIOEKLPLIGSSA	549
Db	498	TNTVTVQGLGAGAIYVQYRARTVAGYGRSGSKMFQMTAEVQTSIOEKLPLIVSSA	557
QY	550	AGLVPLIAVVVIAIVCNRGFEPRADSEYTDKLQHTSGHMTPGMKIYIDPPTYEDPNEAV	609
Db	558	AGLVPLIAVVVIAIVCNRGFEPRADSEYTDKLQHTSGHMTPGMKIYIDPPTYEDPNEAV	617
QY	610	REFAKEIDISCVKIEQVIGAGEFGYCGSHLKPCKREIIPVAITIKSGYTEKORPFLS	669
Db	618	REFAKEIDISCVKIEQVIGAGEFGYCGSHLKPCKREIIPVAITIKSGYTEKORPFLS	677
QY	670	EASIMGQFDHPNVIHLEGVITKSTPYMITTEFENSGISDSFLRQNDGFTVIQVGMRLG	729
Db	678	EASIMGQFDHPNVIHLEGVITKSTPYMITTEFENSGISDSFLRQNDGFTVIQVGMRLG	737
QY	730	IAAGMTYILDNMYVHDLAARNILVNSUVCYGVSPFGSLREDDTSPPTYSLGKIP	789
Db	738	IAAGMTYILDNMYVHDLAARNILVNSUVCYGVSPFGSLREDDTSPPTYSLGKIP	797
QY	790	IRMTAEBAIQYRKFTSASDVMSYGIYVMEVMSYGERPYMDNTQDVINALIEOYRLPEPM	849
Db	798	IRMTAEBAIQYRKFTSASDVMSYGIYVMEVMSYGERPYMDNTQDVINALIEOYRLPEPM	857
QY	850	DCPSALHQLMLDWCQKDRNHRKFCQIYNTLDDKMIKRNFSIKAPAPLSSGINPLEDRTI	909
Db	858	DCPSALHQLMLDWCQKDRNHRKFCQIYNTLDDKMIKRNFSIKAPAPLSSGINPLEDRTI	917
QY	910	PDTSTNTVDENLEAIKMGQYKESFANAGFTSPVDSQMMMEDILRVGVLTAHQKKILN	969
Db	918	PDTSTNTVDENLEAIKMGQYKESFANAGFTSPVDSQMMMEDILRVGVLTAHQKKILN	977
QY	970	SIQVRAQMNQIOQVE	985
Db	978	SIQVRAQMNQIOQVE	993
RESULT 6			
AAAR87018			
ID	AAAR87018 standard; protein; 994 AA.		
XX	AAAR87018;		
AC	AAAR87018;		
XX	DT 19-MAR-1996 (first entry)		
DE	Receptor tyrosine kinase (neural kinase).		
KM	Receptor tyrosine kinase; neural kinase; Nuk; axon; axonogenesis;		
XX	nerve disorder.		
OS	Mus musculus.		
Key	Location/Qualifiers		
PH			

Query Match	92.0%; Score 5125; DB 2; Length 994;	Best Local Similarity 99.5%; Pred. No. 0;	Matches 97%; Conservative 4; Mismatches 1; Indels 0; Gaps 0
10	LLLLPILAAVEETLMDSTTAAELAGMWHPPSGMEVSGYDENMNTIRTYOVNVESSQ	69	
18	LLLLPILAAVEETLMDSTTAAELAGMWHPPSGMEVSGYDENMNTIRTYOVNVESSQ	77	
70	NNMLRTKFIARRGAHRIHVEKKFSYRDOSISIPVPGSCKCTFNLYYYEADFPDATKTPFN	129	
78	NNMLRTKFIARRGAHRIHVEKKFSYRDOSISIPVPGSCKCTFNLYYYEADFPDATKTPFN	137	
130	WMENPMVAKVDITIAADESPSYVDLGRVWKINTETVRSFGPVSRNGFYLAFOYGGCMSLTA	189	
138	WMENPMVAKVDITIAADESPSYVDLGRVWKINTETVRSFGPVSRNGFYLAFOYGGCMSLTA	197	
190	VRFVYKCKRIIIONCAIFOETLSGAESESTLVAARGSCITAAEEVDVPIKLYCNGDGEMLY	249	
198	VRFVYKCKRIIIONCAIFOETLSGAESESTLVAARGSCITAAEEVDVPIKLYCNGDGEMLY	257	
250	PIGRCKACGAFEAENVGIVCRGSGSTGTFKANKQGDCACTHCPINISRTTSGCAINVCRCNGY	309	

Db 258 PIGCMCKAGFEAVENGTVCRGCGPSGTFKANOQDEACTHCPINSRTTSBGATNCVCRNGY 317  
Qy 310 YRADLDLDPCTTISAPQAVISVNETSLMLEWTPPRDSGREDLVYNIICKSGSGSR 369  
Db 318 YRADLDLDPCTTISAPQAVISVNETSLMLEWTPPRDSGREDLVYNIICKSGSGSR 377  
Qy 370 GACTRCGDNVQVAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFSPQFASVNI 429  
Db 378 GACTRCGDNVQVAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFSPQFASVNI 437  
Qy 430 TTMQAPSAVSIMQVSRVDSITLMSQPDQNGVILDELYEKEKELSEYNATAIKSP 489  
Db 438 TTMQAPSAVSIMQVSRVDSITLMSQPDQNGVILDELYEKEKELSEYNATAIKSP 497  
Qy 490 TMTVTVOGLKAGAIYVFOVARTVAGYGRYSGRMVFTQMTAEAYQTSIOEKLPLIIGSSA 549  
Db 498 TMTVTVOGLKAGAIYVFOVARTVAGYGRYSGRMVFTQMTAEAYQTSIOEKLPLIIGSSA 557  
Qy 550 AGVFLIYVAVIIVCNRRGFERADSEYTDKLOHYTSGHMTPMKTIYIDPFYEDPNEAV 609  
Db 558 AGVFLIYVAVIIVCNRRGFERADSEYTDKLOHYTSGHMTPMKTIYIDPFYEDPNEAV 617  
Qy 610 REPAKEIDISCVIEQVIGAGEFEGVCSGHLKPGKREIFVAIKTKSGYTEKQKRDPLS 669  
Db 618 REPAKEIDISCVIEQVIGAGEFEGVCSGHLKPGKREIFVAIKTKSGYTEKQKRDPLS 677  
Qy 670 EASIMGFDPHNVILLEGVTKSTPVMITTEFMENGLDSFLRQNDQGFVTIQLVGMURG 729  
Db 678 EASIMGFDPHNVILLEGVTKSTPVMITTEFMENGLDSFLRQNDQGFVTIQLVGMURG 737  
Qy 730 IAAQMKYLAQMYVHRDLAARNILVNSNLVCKVSDGLSPFEDDPSDPYTSALGCKTP 789  
Db 738 IAAQMKYLAQMYVHRDLAARNILVNSNLVCKVSDGLSPFEDDPSDPYTSALGCKTP 797  
Qy 790 IRTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPMDTINQDYINAEQDYRLPPPM 849  
Db 798 IRTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPMDTINQDYINAEQDYRLPPPM 857  
Qy 850 DCSALHQLMLDCWQCDRNRHPRKFGQIVNLDKXINRPNLSLKMAPSSGINPLIDRTI 909  
Db 858 DCSALHQLMLDCWQCDRNRHPRKFGQIVNLDKXINRPNLSLKMAPSSGINPLIDRTI 917  
Qy 910 PDTSFTVDEMTEAIKMGQYKESFANAGFTSPDVSSOMMEDILRYGVTLAHOCKIIN 969  
Db 918 PDTSFTVDEMTEAIKMGQYKESFANAGFTSPDVSSOMMEDILRYGVTLAHOCKIIN 977  
Qy 970 SIOVMPAQMNOIOSVE 985  
Db 978 SIOVMPAQMNOIOSVE 993

RESULT 7  
AAR85089  
ID AAR85089 standard; protein; 970 AA.  
XX AAR85089;  
AC AAR85089;  
XX  
DT 16-APR-1996 (first entry)  
XX  
DE EPH-like receptor protein tyrosine kinase HEK5.  
XX  
XX EPH-like receptor protein tyrosine kinase; PTK; HEK5;  
KM human eph-like kinase; therapy; diagnosis; vector; antibody.  
XX  
XX Homo sapiens.  
XX  
XX W09528484-A1.  
XX  
XX 26-OCT-1995.  
PD  
PF 14-APR-1995; 95MO-US004681.  
XX

PR 15-APR-1994; 94US-00229509.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Fox GM, Welcher AA, Jing S;  
PI  
XX WPI: 1995-373799/48.  
DR  
XX N-PSDB; AAT02946.  
DR  
XX  
XX New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and  
PT related vectors, host cells, proteins, antibodies etc., used  
PT diagnostically and therapeutically to modulate receptor activation or  
PT prodn.  
XX  
XX  
PS Claim 18; Page 46-49; 133pp; English.  
XX  
XX  
CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,  
CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following  
CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain  
CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the  
CC catalytic domain of chicken EPH-like receptors Cex3, Cex7 and Cex8. HEK11  
CC shows no homology to any known EPH-like receptor. Recombinant HEK  
CC receptors (or their soluble extracellular domains) are produced by  
CC expression of encoding sequences in prokaryotic or eucaryotic host cells,  
CC and are used to produce antibodies (utilised in diagnostic assays) or to  
CC identify and purify ligands for HEK receptors, or therapeutically to  
CC modulate the activation of cell-associated receptors. Soluble HEK  
CC receptor may affect primarily brain and pancreatic cells  
XX  
SQ Sequence 970 AA;  
Query Match 91.4%; Score 5092; DB 2; Length 970;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

15 LAAVEETLMDSTTATAEELGMVHPSPSGMEVSGYDENMTIRTYQVNVFESSQNNMLR 74  
1 LAAVEETLMDSTTATAEELGMVHPSPSGMEVSGYDENMTIRTYQVNVFESSQNNMLR 60  
Qy 75 TKFIRRRGAHRIHVMEKSVRDCSSIPSPVSCKETFMVLYYEADPDSATKTFPMWENP 134  
Db 61 TKFIRRRGAHRIHVMEKSVRDCSSIPSPVSCKETFMVLYYEADPDSATKTFPMWENP 120  
Qy 135 WKVVDITIADESFSQVDLGGRWKINTEVRSFSPVSRGFLAFQDYGGCSLAVRFFY 194  
Db 121 WKVVDITIADESFSQVDLGGRWKINTEVRSFSPVSRGFLAFQDYGGCSLAVRFFY 180  
Qy 195 RKCPRIIONGAIFOETLSGAESTSLVAARSGCINAAEEVDVPIKLYCNGDSEMLVPIERC 254  
Db 181 RKCPRIIONGAIFOETLSGAESTSLVAARSGCINAAEEVDVPIKLYCNGDSEMLVPIERC 240  
Qy 255 MCKAGFEAVENGTVCRGCGPSGTFKANOQDEACTHCPINSRTTSBGATNCVCRNGYRADL 314  
Db 241 MCKAGFEAVENGTVCRGCGPSGTFKANOQDEACTHCPINSRTTSBGATNCVCRNGYRADL 300  
Qy 315 DELDMPCTTISAPQAVISVNETSLMLEWTPPRDSGREDLVYNIICKSGSGGACTR 374  
Db 301 DELDMPCTTISAPQAVISVNETSLMLEWTPPRDSGREDLVYNIICKSGSGGACTR 360  
Qy 375 CGDNVQVAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFSPQFASVNIITNQA 434  
Db 361 CGDNVQVAPROLGLTEPRITISDLLAHTQYTFEIOAVNGVTDQSPFSPQFASVNIITNQA 420  
Qy 435 APSAVSIMQVSRVDSITLMSQPDQNGVILDELYEKEKELSEYNATAIKSPNTVT 494  
Db 421 APSAVSIMQVSRVDSITLMSQPDQNGVILDELYEKEKELSEYNATAIKSPNTVT 480  
Qy 495 VQGLKAGAIYVFOVARTVAGYGRYSGRMVFTQMTAEAYQTSIOEKLPLIIGSSAAGLVF 554  
Db 481 --GLKAGAIYVFOVARTVAGYGRYSGRMVFTQMTAEAYQTSIOEKLPLIIGSSAAGLVF 538  
Qy 555 LIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPMKTIYIDPFYEDPNEAVREFAK 614

Db 539 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598  
QY 615 EIDISCVKIEQVIGAGFEVCSGHLKLPGRREIFVAIKTLKSGYTEKORDFLEASIM 674  
Db 599 EIDISCVKIEQVIGAGFEVCSGHLKLPGRREIFVAIKTLKSGYTEKORDFLEASIM 658  
QY 675 GQFDHPVVIHLEGVVTKSTPVMITTEFMENGSLDSFLRQNDGQFTVIOIVGMLRGIAAGM 734  
Db 659 GQFDHPVVIHLEGVVTKSTPVMITTEFMENGSLDSFLRQNDGQFTVIOIVGMLRGIAAGM 718  
QY 735 KYLDAMNYVHRDLAARNILVNSNLCVSPDGLSRFLEDDTSDPTYSALGKIPIRMTA 794  
Db 719 KYLDAMNYVHRDLAARNILVNSNLCVSPDGLSRFLEDDTSDPTYSALGKIPIRMTA 778  
QY 795 PEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 854  
Db 779 PEAIQYRKFTSASDVMSYGIWMMEVMSYGERPYWDMTNQDVINAIEQDYRLPPMDCPSA 838  
QY 855 LHQIMLDCWQKDRNHRPKFGQIVNTLDKXIRNPNSLKAMAPLSSGINLPILDRITPDYTS 914  
Db 839 LHQIMLDCWQKDRNHRPKFGQIVNTLDKXIRNPNSLKAMAPLSSGINLPILDRITPDYTS 898  
QY 915 FNTVDENLEAIKMGQYKESFANAGFTSFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 974  
Db 899 FNTVDENLEAIKMGQYKESFANAGFTSFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 958  
QY 975 RAQNMNIOISYE 985  
Db 959 RAQNMNIOISYE 969

Search completed: August 28, 2004, 04:08:46  
Job time : 106.415 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: August 28, 2004, 04:05:25 ; Search time 24.814 Seconds  
(without alignments)  
2195.179 Million cell updates/sec

Title: US-09-914-883-4

Perfect score: 5571

Sequence: 1 MARRRGAALLLLPLLAAYE.....QGIFKEDSHKESNDSCGG 1055

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%  
Maximum Match 100%

Listing first 45 summaries

## Database:

Issued Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5129	92.1	994	3	US-08-542-635-2
2	5092	91.4	970	2	US-08-449-645A-11
3	5092	91.4	970	2	US-08-702-367A-11
4	5092	91.4	970	5	PCT-US95-04681-11

## ALIGNMENTS

RESULT 1  
US-08-542-635-2  
Sequence 2, Application US/08542635

Patent No. 6218356

GENERAL INFORMATION:

APPLICANT: Pawson, Anthony  
APPLICANT: Henkemeyer, Mark

APPLICANT: Lecwin, Kenneth

TITLE OF INVENTION: NOVEL NEURAL RECEPTOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Bereskin & Parr

STREET: 40 King Street West, Box 401

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 3Y2

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/542,635  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Mediarmid, Shona S.  
REGISTRATION NUMBER: 38,798  
REFERENCE/DOCKET NUMBER: 3153-162  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398  
TELEX: 06-23115  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
DEVELOPMENTAL STAGE: Embryo  
IMMEDIATE SOURCE:  
LIBRARY: lambda g10 cDNA library  
CLONE: Combined pNURACE A2 and K2 and cDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Distal end of chromosome 4  
MAP POSITION: near the and-1 mutation  
US-08-542-635-2

Query Match 92.1%; Score 5129; DB 3; Length 994;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 972; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY	10	LLLPPLAAVEETLMDSTTATATAGMWHPPSGMEVSGYDENNTTTRYOVAVFESQ	69
DB	18	LLLPPLAAVEETLMDSTTATATAGMWHPPSGMEVSGYDENNTTTRYOVAVFESQ	77
QY	70	NNWLRTKPIRRRGARRHVENKFSVRDCSSIPSVGSKETFNLYYYHADPDAITKTFPN	129
DB	78	NNWLRTKPIRRRGARRHVENKFSVRDCSSIPSVGSKETFNLYYYHADPDAITKTFPN	137
QY	130	WMENWVAVDITLADDESFOVDLGRVWKINTVEASRGFVRSRGFYLAFOYSGCMSLIA	189
DB	138	WMENWVAVDITLADDESFOVDLGRVWKINTVEASRGFVRSRGFYLAFOYSGCMSLIA	197
QY	190	VRFVFRKCPRIITONGALFOETLSGAEISTLVARSGCIANAEVDVPKILYCNBGEMLV	249
DB	198	VRFVFRKCPRIITONGALFOETLSGAEISTLVARSGCIANAEVDVPKILYCNBGEMLV	257
QY	250	PIGRMCAGFEAVENGVCGCGSGTFRKANOGDEACTHCINRTTSEGTNCVCRNGY	309
DB	258	PIGRMCAGFEAVENGVCGCGSGTFRKANOGDEACTHCINRTTSEGTNCVCRNGY	317
QY	310	YRADLDPDMCTTTPSPQAVISSVNETSLMLWTTPRDSGREDLVYNIICKSCSGSR	369
DB	318	YRADLDPDMCTTTPSPQAVISSVNETSLMLWTTPRDSGREDLVYNIICKSCSGSR	377
QY	370	GACTRCGNVOYAPBQGLTEPRITYSLDLAHTQYTFEIQAVNGVTDOSPSPQFASVNI	429
DB	378	GACTRCGNVOYAPBQGLTEPRITYSLDLAHTQYTFEIQAVNGVTDOSPSPQFASVNI	437
QY	430	TTNOAPSAVSIIMOVSRIVDSITLSWQPDQPGVILIDYLOYYEKLSYNTATKSP	489
DB	438	TTNOAPSAVSIIMOVSRIVDSITLSWQPDQPGVILIDYLOYYEKLSYNTATKSP	497
QY	490	TNTVTVOGLKAGATVYFQVRRATVAGVYSGKMYFQTMTEAEVQTSIQEKLPLIIGSSA	549

Db 498 TMTVTGGLAGALIVFQVAAKTVAGYGRYSGLKVFQTMTEAEYQTSIKELPLIYGSSA 557  
QY 550 AGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAV 609  
Db 558 AGVFLIAVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAV 617  
QY 610 REPAKEIDISGVKEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPFS 669  
Db 618 REPAKEIDISGVKEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPFS 677  
QY 670 EASIMGQFDPHNVTHLEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRG 729  
Db 678 EASIMGQFDPHNVTHLEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRG 737  
QY 730 IAGMKYLAAMNYHRLAARNILVNSNLVCKVSDGLSFLEDDTSDPTYSALGKLP 789  
Db 738 IAGMKYLAAMNYHRLAARNILVNSNLVCKVSDGLSFLEDDTSDPTYSALGKLP 797  
QY 790 IRMTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAIEDYRLPPM 849  
Db 798 IRMTAPEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAIEDYRLPPM 857  
QY 850 DCSALHQLMLDCMQDRNRHPRFGQIVNTLDKMRNPNSLKMAFLSSGINLPILDRIT 909  
Db 858 DCSALHQLMLDCMQDRNRHPRFGQIVNTLDKMRNPNSLKMAFLSSGINLPILDRIT 917  
QY 910 PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILN 969  
Db 918 PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILN 977  
QY 970 SIQVRAQNMQIOSVE 985  
Db 978 SIQVRAQNMQIOSVE 993

## RESULT 2

US-08-449-645A-11  
Sequence 11, Application US/08449645A  
Patent No. 5981245  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,645A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-449-645A-11

Query March 91.4%; Score 5093; DB 2; Length 970;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;  
QY 15 LIAAEEETLMDSATTAELMGMMHPPSGMEVSGYDENMTIRIYQVCNPFESSQNMWR 74  
Db 1 LIAAEEETLMDSATTAELMGMMHPPSGMEVSGYDENMTIRIYQVCNPFESSQNMWR 60  
QY 75 TKFIRRGASHIHMEKFSVADCSIPSVPSCKETENLYYEADPDSAKTFPFNMENP 134  
Db 61 TKFIRRGASHIHMEKFSVADCSIPSVPSCKETENLYYEADPDSAKTFPFNMENP 120  
QY 135 WKVADTIADESSFSQVLDGRVWKINTEVRSFGFVSSSGFYLAFOQYGGCSLIAVEFY 194  
Db 121 WKVADTIADESSFSQVLDGRVWKINTEVRSFGFVSSSGFYLAFOQYGGCSLIAVEFY 180  
QY 195 RKCPRIIONGAIPEETLSGAESTSLVAARSGCIANAEVVPKILYCNBGMELVPIGRG 254  
Db 181 RKCPRIIONGAIPEETLSGAESTSLVAARSGCIANAEVVPKILYCNBGMELVPIGRG 240  
QY 255 MCKAGFEAVENGIVCRGCPSGTFKANGDEACTHCPINSRTTSGATNCVCRNGYRADL 314  
Db 241 MCKAGFEAVENGIVCRGCPSGTFKANGDEACTHCPINSRTTSGATNCVCRNGYRADL 300  
QY 315 DPLMPCTTIPSAQAVIISVNETSLMLEWTPPDSGGRDLVYNIICKSGSGRGACTR 374  
Db 301 DPLMPCTTIPSAQAVIISVNETSLMLEWTPPDSGGRDLVYNIICKSGSGRGACTR 360  
QY 375 CGDNVQAPRQLGLTEPRIVISDLAHTQYTFEIOAVNGVTDOSPSPQASVNIITNOA 434  
Db 361 CGDNVQAPRQLGLTEPRIVISDLAHTQYTFEIOAVNGVTDOSPSPQASVNIITNOA 420  
QY 435 APSASIMHQVSRVDSITLSMSQDPDNGVILDYELQYKEKLESENAATAISPTMTYV 494  
Db 421 APSASIMHQVSRVDSITLSMSQDPDNGVILDYELQYKEKLESENAATAISPTMTYV 480  
QY 495 VQGLKAGAIYFQYRARTVAGYGRYSGLKVFQTMTEAEYQTSIOEKLPLIIGSSAGLVF 554  
Db 481 --GLKAGAIYFQYRARTVAGYGRYSGLKVFQTMTEAEYQTSIOEKLPLIIGSSAGLVF 538  
QY 555 LIAAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAVPEFAK 614  
Db 539 LIAAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPGMKIYIDPFYEDNEAVPEFAK 598  
QY 615 EIDISGVKEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPFLSEASIM 674  
Db 599 EIDISGVKEGVIGAGEFGEVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDPFLSEASIM 658  
QY 675 GQFDPHNVTHLEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRGIAAGM 734  
Db 659 GQFDPHNVTHLEGVVTKSTPVMIIIEFMENGLSDSFLRQNDGQFTVIQVLMRGIAAGM 718  
QY 735 KYLADMMYVHRDLAARNILVNSNLVCKVSDGLSFLEDDTSDPTYSALGKLPIMRTA 794  
Db 719 KYLADMMYVHRDLAARNILVNSNLVCKVSDGLSFLEDDTSDPTYSALGKLPIMRTA 778  
QY 795 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAIEDYRLPPMDCPSA 854  
Db 779 PEAIQYRKFTSASDVMSYGIWMEVMSYGERPYWDMTNQDVINAIEDYRLPPMDCPSA 838  
QY 855 LHQIMLDCMQDRNRHPRFGQIVNTLDKMRNPNSLKMAFLSSGINLPILDRITPYYS 914  
Db 839 LHQIMLDCMQDRNRHPRFGQIVNTLDKMRNPNSLKMAFLSSGINLPILDRITPYYS 898  
QY 915 FNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILNSIQVM 974  
Db 899 FNTVDEWLEAIKMGQYKESFANAGFTSPDVVSQMMMEDILRVGVTLAGHQKILNSIQVM 956  
QY 975 RAQNMQIOSVE 985  
Db 959 RAQNMQIOSVE 969

RESULT 3  
US-08-702-367A-11

Sequence 11, Application US/08702367A  
Patent No. 5991246  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-367A-11

Query Match 91.4%; Score 5092; DB 2; Length 970;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 15 LIAAEEITMDSTTAATAGLGMVHPPSGMEVSGYDENMATTRTTYOVCAVFPSSQNNMLR 74  
DB 1 LIAAEEITMDSTTAATAGLGMVHPPSGMEVSGYDENMATTRTTYOVCAVFPSSQNNMLR 60  
QY 75 TKFIRRGARHIVENKESFVDCSSIPSVGSKETFNLYYEADPDSATKTPNNMNEP 134  
DB 61 TKFIRRGARHIVENKESFVDCSSIPSVGSKETFNLYYEADPDSATKTPNNMNEP 120  
QY 135 WVKVDITIADESPQVDLGRVWVKINTEVRSFGVRSRSGFYLAFOYGGCMSLIAVRFY 194  
DB 121 WVKVDITIADESPQVDLGRVWVKINTEVRSFGVRSRSGFYLAFOYGGCMSLIAVRFY 180  
QY 195 RKPRTIIONGAIQOETLSGAEFSTLVAARSCCTANAEVDVPTKLYCNGDGEVLPTIGSC 254  
DB 181 RKPRTIIONGAIQOETLSGAEFSTLVAARSCCTANAEVDVPTKLYCNGDGEVLPTIGSC 240  
QY 255 MCAAGEAVENGTVCGCPGTFKANOGDEACTHCPIINSTRITSEGATNCVCRNGYRADL 314  
DB 241 MCAAGEAVENGTVCGCPGTFKANOGDEACTHCPIINSTRITSEGATNCVCRNGYRADL 300  
QY 315 DPLDMPCTTTPSAPOAVISSVNTSLMLEWTPPRDSCGRDLVYNTICSCSGGRACR 374  
DB 301 DPLDMPCTTTPSAPOAVISSVNTSLMLEWTPPRDSCGRDLVYNTICSCSGGRACR 360  
QY 375 CGDNVOYAPQOLGTEPRYISDILAHYQTFPIQANGVTPDOSPPSPQASVNTTNOA 434  
DB 361 CGDNVOYAPQOLGTEPRYISDILAHYQTFPIQANGVTPDOSPPSPQASVNTTNOA 420  
QY 435 APSAVSIMHGVSRVDSITLSWQPDQPNGVIIIDYELQYEEKLSEYNATAIKSPNTVT 494  
DB 421 APSAVSIMHGVSRVDSITLSWQPDQPNGVIIIDYELQYEEKLSEYNATAIKSPNTVT 480  
QY 495 VOGKAGATVFCVRAATVAGYRGSGWYFQMTTEAVQTSIQKLPILIGSAGLVY 554  
DB 481 VOGKAGATVFCVRAATVAGYRGSGWYFQMTTEAVQTSIQKLPILIGSAGLVY 538

QY 555 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPEMKIYIDPPTVEDPNEAVREFAK 614  
DB 539 LIAVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTPEMKIYIDPPTVEDPNEAVREFAK 598  
QY 615 BIDISCVKIEQVITAGFEGYVCSGHLKLPGRKEIFVAIKLKSGYTKORRDLFSEASIM 674  
DB 599 BIDISCVKIEQVITAGFEGYVCSGHLKLPGRKEIFVAIKLKSGYTKORRDLFSEASIM 658  
QY 675 GQFHPNVVHLEGVVTSTPMITTEPMENGSLDSFLRNDGQFTVQLVGMRLGIAAGM 734  
DB 659 GQFHPNVVHLEGVVTSTPMITTEPMENGSLDSFLRNDGQFTVQLVGMRLGIAAGM 718  
QY 735 KYLADNMYVHEDLAARNILVNSNLVCKVSPGLSRFLEDTSPTTYTSAIGKIPRWTA 794  
DB 719 KYLADNMYVHEDLAARNILVNSNLVCKVSPGLSRFLEDTSPTTYTSAIGKIPRWTA 778  
QY 795 PEALQYRKFTSASVWSYGIWMEVMSYGRPYMDTNQVINAIEDYRLPPEMDCPSA 854  
DB 779 PEALQYRKFTSASVWSYGIWMEVMSYGRPYMDTNQVINAIEDYRLPPEMDCPSA 838  
QY 855 LHQLMDCWQKDRNHRPFQIVNTLDKXIRNPNSLKAMAPLSSGINLPILDRITPDYTS 914  
DB 839 LHQLMDCWQKDRNHRPFQIVNTLDKXIRNPNSLKAMAPLSSGINLPILDRITPDYTS 898  
QY 915 FNTYDEMTLAIKGOYKESFANAGFTSPDYVSQMMEDILRVGYTLAGHOKKILINSIQM 974  
DB 899 FNTYDEMTLAIKGOYKESFANAGFTSPDYVSQMMEDILRVGYTLAGHOKKILINSIQM 958  
QY 975 RAQMNQIOSVE 985  
DB 959 RAQMNQIOSVE 969

RESULT 4  
PCT-US95-04681-11  
Sequence 11, Application PC/TUS9504681  
GENERAL INFORMATION:

APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-04681-11

Query Match 91.4%; Score 5092; DB 5; Length 970;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 967; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 15 LLAABEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYOVCVNFESSQNNMLR 74  
Db 1 LLAABEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYOVCVNFESSQNNMLR 60  
QY 75 TKFRRRGARIRIHVEMFESVRDCSITPSVPSCKETFNLYYEADPDSATKTPNMENP 134  
Db 61 TKFRRRGARIRIHVEMFESVRDCSITPSVPSCKETFNLYYEADPDSATKTPNMENP 120  
QY 135 WVKVDTIADESSFOVDLGRVWKINTEVASFGPVSRSGFYLAFOYGGCMLIAVRVY 194  
Db 121 WVKVDTIADESSFOVDLGRVWKINTEVASFGPVSRSGFYLAFOYGGCMLIAVRVY 180  
QY 195 RKCRRITQNGAIFQETLSGABSTLVAAKSCIANAEVDVPIKLYCNGDEWLPVIGRC 254  
Db 181 RKCRRITQNGAIFQETLSGABSTLVAAKSCIANAEVDVPIKLYCNGDEWLPVIGRC 240  
QY 255 MCKAGFEAVENGTVCRGCPSGTFRKANGDEACTHCPINSRTSEGATNCVCRRNGYRADL 314  
Db 241 MCKAGFEAVENGTVCRGCPSGTFRKANGDEACTHCPINSRTSEGATNCVCRRNGYRADL 300  
QY 315 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTR 374  
Db 301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPRDSGGREDLVYNIICKSCSGRGACTR 360  
QY 375 CGDNVOYAPROGLTEPRYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNIITNOA 434  
Db 361 CGDNVOYAPROGLTEPRYISDLAHTQYTFEIOAVNGVTDQSPSPQFASVNIITNOA 420  
QY 435 APSAVSIMHOVSRTVDSITLSMSQDPQNGVILDYELQYEEKELSEYNAITAKSPNTVT 494  
Db 421 APSAVSIMHOVSRTVDSITLSMSQDPQNGVILDYELQYEEKELSEYNAITAKSPNTVT 480  
QY 495 VOGKXGAIYVFOVARTVAGYRGYSKXYFOJMTAEYOTSIOEKLPLIGSSAGLVF 554  
Db 481 - -GKAGAIYVFOVARTVAGYRGYSKXYFOJMTAEYOTSIOEKLPLIGSSAGLVF 538  
QY 555 LIAVVYIAIVCNRRGERADSEYTDKLOHYTSGMTGPKKIYIDPTYEDPNEAVREPAK 614  
Db 539 LIAVVYIAIVCNRRGERADSEYTDKLOHYTSGMTGPKKIYIDPTYEDPNEAVREPAK 598  
QY 615 EIDISCVKIEHOVIGABEFGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORPFLSEASIM 674  
Db 599 EIDISCVKIEHOVIGABEFGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORPFLSEASIM 658  
QY 675 GQFDHPVILHEGVVKTPTVMITTEFMENGSLDSFLRONDOQFTYIQLVGMLRGIAAGM 734  
Db 659 GQFDHPVILHEGVVKTPTVMITTEFMENGSLDSFLRONDOQFTYIQLVGMLRGIAAGM 718  
QY 735 KYLDANVYVRDLAARNILVNSNLVCKVSDPGLSRFLBDTSDPTYTSLAGKIPIRMTA 794  
Db 719 KYLDANVYVRDLAARNILVNSNLVCKVSDPGLSRFLBDTSDPTYTSLAGKIPIRMTA 778  
QY 795 PEAIORYKFTSASDVMSYGIVMMEVMSYGERPYWMDTNODVINATBQDYRLPPMDCPSA 854  
Db 779 PEAIORYKFTSASDVMSYGIVMMEVMSYGERPYWMDTNODVINATBQDYRLPPMDCPSA 838  
QY 855 LHOJLMDCWQKDRNHRPKFGQIVNLDKXI RNPNLSLKAMAPLSSGINPLLDRTTIDYTS 914  
Db 839 LHOJLMDCWQKDRNHRPKFGQIVNLDKXI RNPNLSLKAMAPLSSGINPLLDRTTIDYTS 898  
QY 915 ENTVDKMLBAIKMGOKYESFANAGFTSPVVSOMMEDILRYGVTLAGHOKKILNSIQVM 974  
Db 899 ENTVDKMLBAIKMGOKYESFANAGFTSPVVSOMMEDILRYGVTLAGHOKKILNSIQVM 958  
QY 975 RAQMNOIQSYVE 985  
Db 959 RAQMNOIQSYVE 969

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Job time : 25.8114 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 28, 2004, 04:08:55 ; Search time 67.1975 Seconds  
(without alignments)  
4939.422 Million cell updates/sec

Title: US-09-914-883-4  
Perfect score: 5571  
Sequence: 1 MALRRLGALLLLPLLAAYE.....QGIFPKDSKESNDCSCGG 1055

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues  
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 90%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications\_AA.\*  
1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/prodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
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16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5571	100.0	1055	16	US-10-648-593-139 Sequence 139, App
2	5170.5	92.8	987	15	US-10-295-027-1193 Sequence 1193, App

ALIGNMENTS

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS  
FILE REFERENCE: D0273 NP  
CURRENT APPLICATION NUMBER: US/10/648,593  
CURRENT FILING DATE: 2003-08-26  
PRIOR APPLICATION NUMBER: 60/406,385  
PRIOR FILING DATE: 2002-08-27  
NUMBER OF SEQ ID NOS: 557  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 139  
LENGTH: 1055  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-648-593-139

Query Match 100.0%; Score 5571; DB 16; Length 1055;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1055; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALRRLGALLLLPLLAAYEETLMDSTTAIAELGMVHPSPGWEVSGYDENNTIRTYQ	60
DB	1	MALRRLGALLLLPLLAAYEETLMDSTTAIAELGMVHPSPGWEVSGYDENNTIRTYQ	60
QY	61	VGNVFESSQNNWLRKFIIRRGAAHRIHVKAFSVRDCSSISVPSGCKETFNLYYEADF	120
DB	61	VGNVFESSQNNWLRKFIIRRGAAHRIHVKAFSVRDCSSISVPSGCKETFNLYYEADF	120
QY	121	DSATKTFPNNMNPVKKVDTIAADESPQVDLGRVKKINTREVSFGVSSGFYLAQD	180
DB	121	DSATKTFPNNMNPVKKVDTIAADESPQVDLGRVKKINTREVSFGVSSGFYLAQD	180
QY	181	YGGCNSLIAYVFRKCRRIIIONGAIFOETLSGABSTSLVARSGCIANAEEVDVPIKLY	240
DB	181	YGGCNSLIAYVFRKCRRIIIONGAIFOETLSGABSTSLVARSGCIANAEEVDVPIKLY	240
QY	241	CNGDESEMLVPIGRGCMCKAFEAVENTGVRGCPGSGTFPANGDEACTHCPINSRTTSGA	300
DB	241	CNGDESEMLVPIGRGCMCKAFEAVENTGVRGCPGSGTFPANGDEACTHCPINSRTTSGA	300
QY	301	TNCVCRNGYRPAADLPDLPDCTTIPSAFOAVISSVNEIISLMEWTPPRDSGREDLVYNI	360
DB	301	TNCVCRNGYRPAADLPDLPDCTTIPSAFOAVISSVNEIISLMEWTPPRDSGREDLVYNI	360
QY	361	ICKSGSGRGACTRGDNVQVAPROLGTEPRITYSDLHATQVTFEIQANGVTDOSPF	420
DB	361	ICKSGSGRGACTRGDNVQVAPROLGTEPRITYSDLHATQVTFEIQANGVTDOSPF	420
QY	421	SPQFASVITITNOAPASAVSIMHQVSRVDSITLSWSQPDOPNGVITDYEIQYEKELSE	480
DB	421	SPQFASVITITNOAPASAVSIMHQVSRVDSITLSWSQPDOPNGVITDYEIQYEKELSE	480
QY	481	YNATAIKSPNTVTYQGLKAGAIYFYQVAPRTVAGYGSIGMTFQMTAEVQTSIEK	540
DB	481	YNATAIKSPNTVTYQGLKAGAIYFYQVAPRTVAGYGSIGMTFQMTAEVQTSIEK	540
QY	541	LPLIIGSSAAGLVFLIAVVVAIAVCNRRGFERADSEYTDKLOHTSGMTEGMYKIIDPF	600
DB	541	LPLIIGSSAAGLVFLIAVVVAIAVCNRRGFERADSEYTDKLOHTSGMTEGMYKIIDPF	600
QY	601	TYEDPNEAVREFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT	660
DB	601	TYEDPNEAVREFAKIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYT	660
QY	661	EKQRDPFISEASIMQFDPHNVITHLEGVTKSTPMVITTEEMENSGIDSPRQNDGQFTV	720
DB	661	EKQRDPFISEASIMQFDPHNVITHLEGVTKSTPMVITTEEMENSGIDSPRQNDGQFTV	720
QY	721	IQVGMGLGIAAGMYLADNMVYHEDLAARNILVNSNLVCKVSPDGLSRFLEDITSDPT	780
DB	721	IQVGMGLGIAAGMYLADNMVYHEDLAARNILVNSNLVCKVSPDGLSRFLEDITSDPT	780
QY	781	TSALGKPIPIRTAEALQYRKFTSASVSVSYGIMMEVMSYGRPPYDMNTQVYINAE	840
DB	781	TSALGKPIPIRTAEALQYRKFTSASVSVSYGIMMEVMSYGRPPYDMNTQVYINAE	840

QY 841 QDYLPPMDCPSALHQLMDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 900  
Db 841 QDYLPPMDCPSALHQLMDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSGI 900  
QY 901 NLPLDRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGTSPDVQOMMEDILRQVTL 960  
Db 901 NLPLDRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGTSPDVQOMMEDILRQVTL 960  
QY 961 AGHQKILINSIQVRAQMNQIQSVGQPLARRPRATGRTKRCOPRVYTKTKCNSNDGKK 1020  
Db 961 AGHQKILINSIQVRAQMNQIQSVGQPLARRPRATGRTKRCOPRVYTKTKCNSNDGKK 1020  
QY 1021 GMGKKTDPGRGREIQGIFKEDSHKESNDCSCG 1055  
Db 1021 GMGKKTDPGRGREIQGIFKEDSHKESNDCSCG 1055

RESULT 2  
US-10-295-027-1193  
Sequence 1193, Application US/10295027  
Publication No. US20030232350A1  
GENERAL INFORMATION:  
APPLICANT: Afari, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt G.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevez, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Marley, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/350,566  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/335,394  
PRIOR FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/332,464  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US 60/334,393  
PRIOR FILING DATE: 2001-11-29  
PRIOR APPLICATION NUMBER: US 60/340,376  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: US 60/347,211  
PRIOR FILING DATE: 2002-01-08  
PRIOR APPLICATION NUMBER: US 60/347,349  
PRIOR FILING DATE: 2002-01-10  
PRIOR APPLICATION NUMBER: US 60/355,250  
PRIOR FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: US 60/356,714  
PRIOR FILING DATE: 2002-02-13  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1386  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1193  
LENGTH: 987  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-295-027-1193

Query Match 92.8%; Score 5170.5; DB 15; Length 987;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 984; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
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Db 1 MALRRLGAAALLLLPLAAVEETLMDSTTATLAEIAGMVAHPSPGWEVSGYDENMTIRTYQ 60  
QY 61 VCNVPESSQNNWLTATKPIRRGCAHRHVEKMFESVRDCSILPSVSGCKETFNLYYADP 120  
Db 61 VCNVPESSQNNWLTATKPIRRGCAHRHVEKMFESVRDCSILPSVSGCKETFNLYYADP 120  
QY 121 DSATKTFPNNMENNPMVKVDTIAADESFQVLDGGRWVKINTEVSSFGVRSRSGFYLAFO 180  
Db 121 DSATKTFPNNMENNPMVKVDTIAADESFQVLDGGRWVKINTEVSSFGVRSRSGFYLAFO 180  
QY 181 YGGCMSLIAVAFYKRCPRITQNGAIFQETLSGAESTSLVAARSGCIANAENDVPIKLY 240  
Db 181 YGGCMSLIAVAFYKRCPRITQNGAIFQETLSGAESTSLVAARSGCIANAENDVPIKLY 240  
QY 241 CNGGEMVLPIGRCMCKAGFEAVENGTVCGCPGSPGCTKANQGDPACTHCPINSTRTEGA 300  
Db 241 CNGGEMVLPIGRCMCKAGFEAVENGTVCGCPGSPGCTKANQGDPACTHCPINSTRTEGA 300  
QY 301 TNCVCRNGYRADDLPDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360  
Db 301 TNCVCRNGYRADDLPDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNI 360  
QY 361 ICKSGSGRGACTCGGNVQAPARQGLTEPRITISDLIAHTQYTFEIQAVNGVTDQSPF 420  
Db 361 ICKSGSGRGACTCGGNVQAPARQGLTEPRITISDLIAHTQYTFEIQAVNGVTDQSPF 420  
QY 421 SPQFASVITITNQAPASVSIHQVSRVDSITLSWQCPQNGVILIDYELQYKELSE 480  
Db 421 SPQFASVITITNQAPASVSIHQVSRVDSITLSWQCPQNGVILIDYELQYKELSE 480  
QY 481 YNATAIKSPNTTAVQGLKAGAIYFQVRAVAGYRSGKMYFQMTAEVQTSIQEK 540  
Db 481 YNATAIKSPNTTAVQGLKAGAIYFQVRAVAGYRSGKMYFQMTAEVQTSIQEK 540  
QY 541 LPLIIGSSAAGLVPLAVVIAIVCN-RRGERADSEYTKLOHYSGHMTPGKIYIDP 599  
Db 541 LPLIIGSSAAGLVPLAVVIAIVCNRRGERADSEYTKLOHYSGHMTPGKIYIDP 599  
QY 600 FTYEDPNEAVEBPKEIDISCKIEQYIGAGEFGEVSCGHLKPGKREIYVAIKTKSGY 659  
Db 600 FTYEDPNEAVEBPKEIDISCKIEQYIGAGEFGEVSCGHLKPGKREIYVAIKTKSGY 659  
QY 661 FTYEDPNEAVEBPKEIDISCKIEQYIGAGEFGEVSCGHLKPGKREIYVAIKTKSGY 660  
Db 661 FTYEDPNEAVEBPKEIDISCKIEQYIGAGEFGEVSCGHLKPGKREIYVAIKTKSGY 660  
QY 720 VIQVGMRLRGIAAGMKYLAADNYYHRDLAARNILVNSNLVCKVSDFLSREFLEDDTSPT 779  
Db 720 VIQVGMRLRGIAAGMKYLAADNYYHRDLAARNILVNSNLVCKVSDFLSREFLEDDTSPT 779  
QY 721 VIQVGMRLRGIAAGMKYLAADNYYHRDLAARNILVNSNLVCKVSDFLSREFLEDDTSPT 780  
Db 721 VIQVGMRLRGIAAGMKYLAADNYYHRDLAARNILVNSNLVCKVSDFLSREFLEDDTSPT 780  
QY 780 YTSALGKIPIRMTAPPAIQKRTSASDVWSYGIWMEVMSYGERPYWMTNODVINAI 839  
Db 780 YTSALGKIPIRMTAPPAIQKRTSASDVWSYGIWMEVMSYGERPYWMTNODVINAI 839  
QY 840 EODYRLPPMDCPSALHQLMDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 899  
Db 840 EODYRLPPMDCPSALHQLMDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 899  
QY 841 EODYRLPPMDCPSALHQLMDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 900  
Db 841 EODYRLPPMDCPSALHQLMDCWQKDNHRPKFGQIVNTLDMKIRNPNSLKAMAPLSSG 900  
QY 900 INPLDRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGTSPDVQOMMEDILRQVTL 959  
Db 900 INPLDRTIPDYTSFNTVDWMLKAIKMGQYKESFANAGTSPDVQOMMEDILRQVTL 959  
QY 960 LAGHQKILINSIQVRAQMNQIQSVG 985  
Db 960 LAGHQKILINSIQVRAQMNQIQSVG 985

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